

RESULT 6						
	ABBR	ABRPR	STANDARD;	PRT;	527 AA.	
Qy	ID	ABRPR	STANDARD;	PRT;	527 AA.	
Db	Q06077:	P81374;				
Db	DT	15-DEC-1998	(Rel. 37, Created)			
Db	DT	15-DEC-2003	(Rel. 37, Last sequence update)			
Db	DE	28-FEB-2003	(Rel. 41, Last annotation update)			
Db	DE	Abriin-b precursor (Contains: Abriin-b A chain (tRNA N-glycosidase) (EC 3.2.2.22); Abriin-b B chain (EC 3.2.2.22))				
Os	OS	Abrius preatorius (Indian liquorice)	(Crab's eye).			
Oc	Oc	Eukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina; Spermatophytina; Magnoliophytina; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Abreuae; Abrus.				
Ox	Ox	[1] NCBI_TAXID=3816;	RN			
Db	RP	SEQUENCE FROM N.A.				

MEDLINE=93132798; PubMed=8421313;	Hung C.-H., Lee M.-C., Lee T.-C., Lin J.-Y.;	"Primary structure of three distinct isoabrinins determined by cDNA sequencing. Conservation and significance.";
[2]	J. Mol. Biol. 229:263-267(1993).	
P	SEQUENCE OF 260-527.	
C	TISSUE=Seed;	
C	MEDLINE=91169023; PubMed=7763422;	
A	Kimura M., Sumizawa T., Funatsu G.;	
A	"The complete amino acid sequences of the B-chains of abrin-a and abrin-b, toxic proteins from the seeds of Abrus precatorius.";	
T	Biochim. Biotechnol. Biochem. 57:1666-1691(1993).	
T	-!- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RNA.	
T	ABRINA A IS MORE TOXIC THAN RICIN.	
T	-!- FUNCTION: THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT FACILITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT PRECEDES ENDOCYTOSIS.	
C	-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at the specific adenine on the 28S rRNA.	
C	-!- SUBUNIT: DISULFIDE LINKED DIMER OF A AND B CHAINS.	
C	-!- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).	
C	-!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.	
C	-!- SIMILARITY: Contains 2 ricin B-type lectin domains.	
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C	EMBL: M98345; AAA32265.1; -.	
R	PIR: S32430; S322430.	
R	HSSP: P11140; IABR.	
R	InterPro: IPR000772; Ricin_B_lectin.	
R	InterPro: IPR001574; RIP.	
R	PFAM: PF00652; Ricin_B_lectin; 6.	
R	Pfam: PF00161; RIP; 1.	
R	PRINTS: PR00396; SHIGARICIN.	
R	SMART: SM00458; RICIN; 2.	
R	PROSTRE: PS50231; RICIN B LECTIN; 2.	
R	PROSTRE: PS00277; SHIGA-RICIN; 1.	
R	Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repressor; Lectin; Pyrrolidine carboxylic acid.	
T	CHAIN 1 250 ABRIN-B A CHAIN.	
T	PEPTIDE 251 260 LINKER PEPTIDE.	
T	CHAIN 261 527 ABRIN-B B CHAIN.	
T	DOMAIN 272 399 RICIN B-TYPE LECTIN 1.	
T	REPEAT 402 526 RICIN B-TYPE LECTIN 2.	
T	DOMAIN 402 527 ACT-SUB	
T	REPEAT 282 324 1-ALPHA.	
T	REPEAT 325 365 1-BETA.	
T	REPEAT 368 400 1-GAMMA.	
T	REPEAT 413 448 2-ALPHA.	
T	REPEAT 452 491 2-BETA.	
T	REPEAT 494 527 2-GAMMA.	
F	ACT-SUB 163 163 BY SIMILARITY.	
F	DISULFID 246 268 INTERCHAIN (BY SIMILARITY).	
F	DISULFID 285 304 BY SIMILARITY.	
F	DISULFID 328 345 BY SIMILARITY.	
F	DISULFID 416 429 BY SIMILARITY.	
F	DISULFID 455 472 BY SIMILARITY.	
F	MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID (BY SIMILARITY).	
F	CARBOHYD 110 110 (POTENTIAL).	
F	CARBOHYD 360 360 (POTENTIAL).	
F	CARBOHYD 400 400 (POTENTIAL).	
F	CONFLECT 282 282 (POTENTIAL).	

RESULT 7			
RIP2_BRYDI	BRYDI	STANDARD;	PRT;
ID P98184	ID P98184; Q9S8J0;		282 AA.
AC			
DT 16-OCT-2001	(Rel. 40, Created)		
DT 16-OCT-2001	(Rel. 40, Last annotation update)		
DT 28-FEB-2003	(Rel. 41, Last annotation update)		
DE Ribosome-inactivating protein bryodin II precursor (rRNA N-glycosidase) (EC 3.2.2.22) (BD2).			
DS Bryonia dioica (Red bryony).			
DS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; euuroids I; Cucurbitales; Cucurbitaceae; Bryoniae.			
NCBI_TaxID=3652;			
[1]			
SEQUENCE FROM N.A.			
SIEGALL C.B., GAWLAK S.L., MARQUARDT H.J.			
"Bryodin 2 a ribosome-inactivating protein isolated from the plant Bryonia dioica";			
Patent number US55597569, 28-JAN-1997.			
[2]			
SEQUENCE OF 22-42.			
TISSUE=Root;			
RA MEDLINE=95151812; PubMed=7849072;			
RA Siegall C.B., Gawlak S.L., Chace D., Wolff E.A., Mixan B., Marquardt H.;			
RA "Characterization of ribosome-inactivating proteins isolated from Bryonia dioica and their utility as carcinoma-reactive immunconjugates.";			
RT Bioconj. Chem. 5:423-429 (1994).			
RT !- FUNCTION: Ribosome-inactivating protein of type 1, inhibits protein synthesis in animal cells (by similarity).			
CC  - CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenine on the 2'8S rRNA.			
CC  - SIMILARITY: Belongs to the RIBOSOME-INACTIVATING PROTEIN FAMILY.			
CC TYPE 1 RIP SUBFAMILY.			
CC			

RESULT 8							
	NIGRIN SAMNI	STANDARD	PRT;	563 AA.			
[1]	ID NIGRIN SAMNI AC P33183; P331184; P93542; DT 01-OCT-1993 (Rel. 27, Created) DT 28-FEB-2003 (Rel. 41, Last sequence update) DT 28-FEB-2003 (Rel. 41, Last annotation update)						
[2]	DE Nigrin b precursor (Aggutinin V) (SNAV) [Contains: Nigrin b A chain (rRNA N-glycosidase) (EC 3.2.2.22); Nigrin b B chain]. OS Sambucus nigra (European elder). OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; OC Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots; OC Asteridae; campanulids; dipsacales; Adoxaceae; Sambucus. NCBI_TaxID=4202;						
RN	SEQUENCE FROM N.A.						
RP	SEQUENCE=Back;						
RC	MEDLINE=94003077; PubMed=8400135;						
RX	Girbes T., Cidores L., Ferreres J.M., Rojo M.A., Iglesias R., Munoz R., Arias F.J., Calonge M., Garcia J.R., Mendez E.; "Isolation and partial characterization of nigrin b, a non-toxic novel type 2 ribosome-inactivating protein from the bark of Sambucus nigra L." ; Plant Mol. Biol., 22:1181-1186(1993).						
RX	"Isolation and partial characterization of nigrin b, a non-toxic novel type 2 ribosome-inactivating protein from the bark of Sambucus nigra L." ; Plant Mol. Biol., 22:1181-1186(1993).						
RX	CC 11. FUNCTION: NON-TOXIC TYPE 2 RIBOZYME WHICH STRONGLY INHIBITS MAMMALIAN						

PROTEIN SYNTHESIS BUT DOES NOT AFFECT PLANT NOR BACTERIAL PROTEIN SYNTHESIS. THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S rRNA. THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT FACILITATES THE BINDING OF NIGRIN B TO THE CELL MEMBRANE THAT PRECEDES ENDOCYTOSIS.

-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.  
 CC -!- SUBUNIT: Disulfide-linked dimer of A and B chains.  
 CC -!- SIMILARITY: In the N-terminal section; belongs to the ribosome-inactivating protein family. Type 2 RIP subfamily.  
 CC -!- SIMILARITY: Contains 2 ricin B-type lectin domains.

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CC DR EMBL; U41299; AAB39475.1; -.  
 CC DR PIR; S37382; S37382.  
 CC DR InterPro; IPR000772; Ricin\_B\_lectin.  
 CC DR InterPro; IPR001574; RIP.  
 CC DR Pfam; PF00552; Ricin\_B\_lectin\_6.  
 CC DR Pfam; PF00161; RIP; 1.  
 CC DR PRINTS; PR00396; SHIGARICIN.  
 CC DR SMART; SM00458; RICIN.  
 CC DR PROSITE; PS00275; SHIGA\_RICIN\_1.  
 CC DR PROSITE; PS50231; RICIN\_B\_LECTIN; 2.  
 KW Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat; Glycoprotein; Lectin; Signal.  
 FT SIGNAL 1 25  
 FT CHAIN 26 297 NIGRIN B A CHAIN.  
 FT CHAIN 298 563 NIGRIN B B CHAIN.  
 FT DOMAIN 305 431 RICIN B-TYPE LECTIN 1.  
 FT DOMAIN 434 559 RICIN B-TYPE LECTIN 2.  
 FT REPEAT 316 356 1-ALPHA.  
 FT REPEAT 357 397 1-BETA.  
 FT REPEAT 400 432 1 GAMMA.  
 FT REPEAT 445 482 2-ALPHA.  
 FT REPEAT 486 524 2-BETA.  
 FT REPEAT 527 554 2-GAMMA.  
 FT ACT SITE 188 198 BY SIMILARITY.  
 FT DISULFID 274 302 INTERCHAIN (BY SIMILARITY).  
 FT DISULFID 319 338 BY SIMILARITY.  
 FT DISULFID 360 377 BY SIMILARITY.  
 FT DISULFID 448 463 BY SIMILARITY.  
 FT DISULFID 489 505 BY SIMILARITY.  
 FT CARBOHYD 221 221 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 368 368 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 376 376 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 483 483 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 537 537 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CONFLICT 39 39 K->V (LN REF. 2).  
 SQ SEQUENCE 563 AA; 62300 MW; F250CBE24621BF14 CRO64;

Query Match Score 307.5; DB 1; Length 563;  
 Best Local Similarity 38.4%; Prd. No. 5.3e-21;  
 Matches 73; Conservative 36; Mismatches 56; Indels 25; Gaps 5;

Qy 6 YPIINFPTAGATQSYTNGNSAYFPHDNQDEAEI---GRLTVPVRGVLPINORETVELSNH 55  
 Qy 56 AEUSVTLAIDLWATMAYVYVAGNSAYFPHDNQDEAEI---GRLTVPVRGVLPINORETVELSNH 55  
 Db 28 YPSVSENLGDASATYRDLSNRKTVATGTYEVNGLPVLRRESEVQYSKSRFLVPLPTNY 87  
 Qy 88 NGNTVTLAVDTNLWYWAESGNANSYFF---KDATEVQKSNLFVGTKQN-TLSFTGNY 141  
 Qy 114 DRLEQLAGNLRENTELNGNPLEEIAASLYYSTGGTQLPTLARSFLCITIONISEAARFQY 173

DB 142 DNLETAANTRRESIELGPSPLDGATSLYHGDI-----SVARSLVVQMVSEAARFRY 194  
 Qy 174 IEGBEMRTR 183  
 DB 195 IEQEVRRSLQ 204

RESULT 9  
 RIPI\_BRIDI\_BRYDI STANDARD; PRT; 290 AA.  
 ID RIPI\_BRIDI; Q9S819;  
 AC P33185; Q9S819;  
 DT 01-OCT-1993 (Rel. 27, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Ribosome-inactivating protein bryodin I precursor (tRNA N-glycosidase) (EC 3.2.2.22) (BDI).  
 OS Bryonia dioica (Red bryony).  
 OC Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eu dicots; eudicots; Rosidae;  
 OC eu rosids I; Cucurbitaceae; Bryonia.  
 NCBI\_TAXID=3652;  
 RN [1]  
 SEQUENCE FROM N.A. AND X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).  
 RP TISSUE-Leaf;  
 RX MEDLINE=97228081; PubMed=9115985;  
 RA Gawlik S.L., Newbauer M., Klei H.E., Chang C.Y.Y., Einspahr H.M., Siegall C.B.;  
 RA "Molecular, biological, and preliminary structural analysis of recombinant bryodin 1, a ribosome-inactivating protein from the plant Bryonia dioica.";  
 RT Biochemistry 36:3095-3103 (1997).  
 RL [2]  
 RP SEQUENCE FROM N.A.  
 RA Siegall C.B.;  
 RT "Cloning and expression of a gene encoding bryodin 1 from Bryonia dioica.";  
 RL Patent number US5541110, 30-JUL-1996.  
 RN [3]  
 RP SEQUENCE OF 24-66.  
 RC TISSUE=Seed;  
 RX MEDLINE=89326651; PubMed=2752596;  
 RA Montecuccchi P.C., Lazzarini A.M., Barbieri L., Stirpe F., Soria M., Lappi D.;  
 RA "N-terminal sequence of some ribosome-inactivating proteins.";  
 RL Int. J. Pept. Protein Res. 33:263-267(1989).  
 RN [4]  
 RP SEQUENCE OF 24-43.  
 RC TISSUE=Root;  
 RX MEDLINE=95151812; PubMed=7849072;  
 RA Siegall C.B., Gawlik S.L., Chace D., Wolff E.A., Mixan B., Margardt H.;  
 RT "Characterization of ribosome-inactivating proteins isolated from Bryonia dioica and their utility as carcinoma-reactive immunoenzyme conjugates";  
 RL Bioconjug. Chem. 5:423-429(1994).  
 -!- FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1, INHIBITS PROTEIN SYNTHESIS IN ANIMAL CELLS.  
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenine on the 28S rRNA.  
 CC -!- PTM: APPEARS TO UNDERGO PROTEOLYTIC CLEAVAGE IN THE C-TERMINAL TO PRODUCE A SHORTER PROTEIN.  
 CC -!- BIOTECHNOLOGY: Especially useful as immunotoxin for pharmacological applications as it has low toxicity in rats and mice but is potent once inside target cells.  
 CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 CC TYPE 1 RIP SUBFAMILY.

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INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.  
 !- SIMILARITY: Contains 2 ricin B-type lectin domains.

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 CC or send an email to license@isb-sib.ch).

CC EMBL; M98344; AAA32644.1; ALT INIT.  
 DR PIR; S32429; T2LSA.  
 DR PDB; 1ABR; 07-FCB-95.  
 DR InterPro; IPR000772; Ricin\_B\_lectin.  
 DR InterPro; IPR001574; RIP.  
 DR Pfam; PF0052; Ricin\_B\_lectin; 6.  
 DR Pfam; PF00161; RIP; 1.  
 DR PRINTS; PR00396; SHGARICIN.  
 DR SMART; SM0458; RICIN; 2.  
 DR PROSITE; PS50231; RICIN\_BLECTIN; 2.  
 DR PROSITE; PS00275; SHIGA\_RICIN; 1.  
 KW Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat;  
 KW Glycoprotein; Lectin; 3D-structure; Pyrrolidone carboxylic acid.

FT CHAIN 1 251 ARRIN-A A CHAIN.  
 FT PEPTIDE 252 LINKER PEPTIDE.  
 FT CHAIN 262 ARRIN-A B CHAIN.  
 FT DOMAIN 273 RICIN B-TYPE LECTIN 1.  
 FT DOMAIN 403 RICIN B-TYPE LECTIN 2.  
 FT REPEAT 283 325 1-ALPHA.  
 FT REPEAT 326 365 1-BETA.  
 FT REPEAT 369 401 1-GAMMA.  
 FT REPEAT 414 449 2-ALPHA.  
 FT REPEAT 453 492 2-BETA.  
 FT REPEAT 495 528 2-GAMMA.  
 FT ACT SITE 164 164 BY SIMILARITY.  
 FT DISULFID 247 269 INTERCHAIN (BY SIMILARITY).  
 FT DISULFID 286 305 BY SIMILARITY.  
 FT DISULFID 329 346 BY SIMILARITY.  
 FT DISULFID 417 430 BY SIMILARITY.  
 FT DISULFID 456 473 BY SIMILARITY.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT CARBOHYD 361 361 N-LINKED (GLCNAC . ).  
 FT CARBOHYD 401 401 MISSING (IN REF. 2).  
 FT CONFLICT 202 202 N -> Y (IN REF. 4).  
 FT CONFLICT 298 298 M -> L (IN REF. 4).  
 FT CONFLICT 427 427 P -> P (IN REF. 4).  
 FT CONFLICT 467 467 V -> L (IN REF. 4).  
 FT STRAND 483 8  
 FT TURN 5 8  
 FT TURN 10 11  
 FT HELIX 14 28  
 FT STRAND 32 33  
 FT TURN 34 35  
 FT STRAND 36 38  
 FT TURN 42 43  
 FT HELIX 47 49  
 FT STRAND 51 57  
 FT STRAND 63 69  
 FT TURN 70 72  
 FT STRAND 75 79  
 FT STRAND 83 86  
 FT TURN 88 89  
 FT TURN 92 93  
 FT HELIX 94 97  
 FT TURN 100 101  
 FT STRAND 103 106  
 FT TURN 113 114  
 FT HELIX 115 119  
 FT TURN 124 126  
 FT STRAND 129 129  
 FT HELIX 131 142

FT TURN 143 144  
 FT HELIX 148 149  
 FT STRAND 168 168  
 FT HELIX 169 180  
 FT TURN 181 182  
 FT STRAND 185 185  
 FT HELIX 189 196  
 FT TURN 197 197  
 FT HELIX 198 207  
 FT STRAND 212 220  
 FT TURN 222 223  
 FT STRAND 226 231  
 FT TURN 232 233  
 FT HELIX 235 239  
 FT STRAND 240 240  
 FT STRAND 243 243  
 FT STRAND 248 248  
 FT STRAND 266 268  
 FT STRAND 276 277  
 FT STRAND 279 280  
 FT HELIX 282 284  
 FT STRAND 286 289  
 FT HELIX 290 292  
 FT TURN 296 297  
 FT STRAND 299 303  
 FT HELIX 311 313  
 FT STRAND 315 317  
 FT TURN 319 320  
 FT STRAND 322 325  
 FT TURN 326 327  
 FT STRAND 328 332  
 FT TURN 337 338  
 FT STRAND 340 344  
 FT TURN 346 348  
 FT HELIX 351 353  
 FT STRAND 355 355  
 FT STRAND 357 358  
 FT TURN 360 361  
 FT STRAND 364 366  
 FT TURN 367 370  
 FT STRAND 371 374  
 FT TURN 380 381  
 FT STRAND 383 383  
 FT STRAND 385 387  
 FT HELIX 393 395  
 FT STRAND 398 399  
 FT STRAND 406 408  
 FT TURN 410 411  
 FT HELIX 413 415  
 FT STRAND 417 421  
 FT TURN 422 423  
 FT STRAND 424 428  
 FT TURN 432 433  
 FT HELIX 435 437  
 FT STRAND 439 441  
 FT TURN 443 444  
 FT STRAND 447 449  
 FT TURN 450 451  
 FT STRAND 452 459  
 FT TURN 464 465  
 FT STRAND 467 472  
 FT TURN 474 475  
 FT HELIX 478 480  
 FT STRAND 483 484  
 FT TURN 486 487  
 FT STRAND 490 492  
 FT TURN 493 496  
 FT STRAND 497 501

Query Match 31.5%; Score 303.5; DB 1; Length 528;  
 Best Local Similarity 41.1%; Pred. No. 1.4e-20;  
 Matches 76; Conservative 26; Mismatches 64; Indels 19; Gaps 5;

QY	9 INFITAGATVQSYTNFIRAVRGRLL-----TVLPNRVGLPINQRFLVELSNHAEV	60
Db	5 IKFSTEGATQSQSYKRFIEARRERGGLIHDIPDPTLQERNRYTVEVSNTDTEI	64
QY	61 TLALITYTNAYVGVGRAGNSAYFF--PDNQEDAAEATHLFTDVQRYTFAFGNNYDRLEQ	118
Db	65 EVGIDTYTNAYVAVTAAAGTOSFLDAPSSA----YLTGT-DQHSLSFYGYTGDLR	118
QY	119 LAGNURENIELNGGLEEAAISALYYSTGTQLPLTARSPICOMISAAARFQYIEGEM	178
Db	119 WAHQSRQQTPIGLQALTHGS---PFRSGENDNEEKARTLIVITQMVBAARFRYISNEY	175
QY	179 RTRIR 183	
Db	176 RVSIQ 180	
<b>RESULT 11</b>		
RIBP_LUFCY	STANDARD;	PRT;
ID	RIBP_LUFCY	250 AA.
AC	P22851	
DT	01-AUG-1991 (Rel. 19, Created)	
DT	28-FEB-2003 (Rel. 41, Last annotation update)	
DE	Ribosome-inactivating protein luffin-B (rRNA N-glycosidase)	
DB	(EC 3.2.2.22).	
OS	Luffa cylindrica (Smooth loofah) (Sponge, gourd)	
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
OC	Spermatophyta; Magnoliophyta; eudicots; Rosidae;	
OC	eurosidos II; Cucurbitales; Cucurbitaceae; Luffa.	
OX	NCBI_TaxID=3670;	
RN	[1]	
RP	SEQUENCE; TISSUE=Seed;	
RX	MLINE=488; PubMed=136866;	
RA	Islam M.R.; Hirayama H.; Funatsu G.	
RT	"Complete amino acid sequence of luffin-b, a ribosome-inactivating protein from sponge gourd (luffa cylindrica) seeds."	
RL	Agric. Biol. Chem. 55:229-238(1991)	
CC	-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenine on the 28S rRNA.	
CC	-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.	
CC	TYPE 1 RIP SUBFAMILY.	
DR	PIR; JN0108; JN0108	
DR	HSSP; P16094; IAHC.	
DR	InterPro; IPR001574; RIP.	
DR	PFAM; PF00161; RIP.	
DR	PRINTS; PR00396; SHIGARICIN.	
DR	PROSITE; PS00375; SHIGA_RICIN.	
DR	Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase; Toxin; Signal.	
FT	CHAIN 1	21
FT	PUTATIVE RIBOSOME-INACTIVATING PROTEIN.	
FT	ACT SITE 185 185 BY SIMILARITY.	
FT	PEPTIDE 103 103 N-LINKED (GLCNAC. . .)	
FT	CARBOHYD 110 110 N-LINKED (GLCNAC. . .)	
FT	CARBOHYD 252 252 N-LINKED (GLCNAC. . .)	
SQ	SEQUENCE 286 AA; 31771 NW; 4EFD4966E604DA41 CRC64;	
<b>Query Match</b>		
QY	9 INFITAGATVQSYTNFIRAVRGRLL-----TVLPNRVGLPINQRFLVELSNHAEV	58
Db	3 VSFSLSGADEKSKYSKFITALRKALPSKEYSVNIPULLPSASGA---SRYLMLQSNYDAK	59
QY	59 SVTLAIDVTVNAYVGVGRAGNSAYFFPHDNOBDAEATHLFTDVQRYTFAFGNNYDRLEQ	118
Db	60 AITMAIDVTNVYIMGYLNSTSYF--ANEDAKIASQYVFKGSTLVTPSGNYERLN	116
QY	119 LAGNURENIELNGGLEEAAISALYYSTGTQLPLTARSPICOMISAAARFQYIEGEM	178
Db	117 AGKIREKIPGFRADSATISIFYDS---TAAAGAVLVIQTTABASRFKTCIEQ1	171
QY	179 RTRIRN 183	
Db	172 IERIPK 178	
<b>RESULT 13</b>		

RIPA\_LUFCY STANDARD; PRT; 277 AA.  
AC ID RIPA\_LUFCY  
AC Q00455;  
DT 01-DEC-1992 (Rel. 24, Created)  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DT 01-FEB-2003 (Rel. 41, Last annotation update)  
DE Ribosome-inactivating protein luffin-alpha precursor (rRNA N-glycosidase) (EC 3.2.2.22).  
DE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Embryophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Cucurbitales; Cucurbitaceae; Momordica.  
OC NCBI\_TaxID:3672;  
RN [1]  
RN SEQUENCE FROM N.A.  
RN TISSUE=Seed;  
RC MEDLINE=92288316; PubMed=1600156;  
RA Kataoka J., Rabuka N., Miyano M., Masuta C., Koiwai A.;  
RT "Nucleotide sequence of cDNA encoding alpha-luffin, a ribosome-inactivating protein from Luffa cylindrica.";  
RL Plant Mol. Biol. 18:1199-1202 (1992).  
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenine on the 28S rRNA.  
CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
CC -!- TYPE 1 RIP SUBFAMILY.  
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CC DR EMBL; Z12175; CA78166.1; -.  
CC DR PIR; S25566; S25560.  
CC DR ICF5; 07-JUN-93.  
CC DR InterPro; IPR001574; RIP.  
CC DR Pfam; PF00111; RIP; 1.  
CC DR PRINTS; PR00396; SHIGARICIN.  
CC DR PROSITE; PS00275; SHIGA\_RICIN.1.  
CC KW Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin; Signal 1 23 RIBOSOME-INACTIVATING PROTEIN MOMORDIN  
CC FT SIGNAL 1 23 RIBOSOME-INACTIVATING PROTEIN MOMORDIN  
CC FT CHAIN 20 277 RIBOSOME-INACTIVATING PROTEIN LUFVIN-  
CC FT ACT SITE 179 179 ALPHA.  
CC SQ SEQUENCE BY SIMILARITY.  
CC 30212 MW; EA17FC22798C25AC CRC64;  
CC 28.4%; Score 274.5; DB 1; Length 286;  
CC Best Local Similarity 33.3%; Pred. No. 3e-18;  
CC Matches 63; Conservative 42; Mismatches 61; Indels 23; Gaps 5;  
CC 9 INFNTGAGATVQSTNFIRAVRGRGLTVLPNRVGLPIN-----QRFILVELSNHAE 57  
CC 22 VRFSLSGSSSTSYSKFGDLR--KALPSN-GTVVNITLLSSASGASRYTMLNSYDG 77  
CC 58 LSUTLADVTNAATVGYGRAGNSAYFFHDNQDAAEATHLFDVQNYTEAGGNDRLE 117  
CC 78 KA-TTVAVAVTNTVYIMGLVNSTVYFF--NESDAKLSAQYFKGSTIVLPGSGNYEKLQ 134  
CC 118 QLAGNLRENTEIENGPLEBAISALYYSTGGTQLPDTARSFTICOMISEAARFYQTEGE 177  
CC 135 TAAGKIREKIPPLGFPAUDSAITLFLHYDS----TAAAAAFLVIIQTTAASRFKTYEQ 189  
CC 178 MTRIRYNR 186  
CC 190 IIERISKNQ 198  
CC RESULT 15  
CC RIPI1\_MOMCH ID RIPI1\_MOMCH STANDARD;  
CC AC P16034; P2497; PRT; 286 AA.  
CC DT 01-APR-1990 (Rel. 14, Created)

01-MAR-1992 (Rel. 21, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)

DR Ribosome-inactivating protein monordin I precursor (tRNA  
 DE N-glycosidase) (EC 3.2.2.22) (Alpha-momorcharin) (Alpha-MMC).  
 DR Monordica charantia (Bitter gourd) (Balsam pear).  
 DR Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Sporopasophytidae; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Cucurbitales; Cucurbitaceae; Momordica.  
 OC NCBI\_TaxID=3673;

OX RP SEQUENCE FROM N.A.

RC MEDLINE=91159486; PubMed=2001404;  
 RA HO W.K.K., Liu S.C., Shaw P.C., Yeung H.W., Ng T.B., Chan W.Y.;  
 RT "Cloning of the cDNA of alpha-momorcharin: a ribosome inactivating  
 protein.";  
 RL Biochim. Biophys. Acta 1088:311-314 (1991).

[2] RP SEQUENCE OF 24-38.

RC TISSUE=Seed;  
 RX MEDLINE=9326691; PubMed=2755196;  
 RA Montecuccchi P.C., Lazzarini A.M., Barbieri L., Stirpe F., Soria M.,  
 RA Lappi D.;  
 RT "N-terminal sequence of some ribosome-inactivating proteins.";  
 RL Int. J. Pept. Protein Res. 33:263-267(1989).

[3] RN RP SEQUENCE OF 24-70.

RC TISSUE=Seed;  
 RX MEDLINE=89005108; PubMed=3262509;  
 RA Casella P., Dussossoy D., Falasca A.I., Barbieri L., Stirpe F.,  
 RA Guillermo J.C., Ferrara P., Bolognesi A., Canini P., Stirpe F.;  
 RT "Trichokirin, a ribosome-inactivating protein from the seeds of  
 RT Trichosanthus kirilowii Maximowicz. Purification, partial  
 RT characterization and use for preparation of immunotoxins.";  
 RL Eur. J. Biochem. 176:581-588(1988).

[4] RN RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).  
 RX MEDLINE=4356447; PubMed=8075985;  
 RA Ren J., Wang Y., Dong Y., Stuart D.I.;  
 RT "The N-glycosidase mechanism of ribosome-inactivating proteins  
 implied by crystal structures of alpha-momorcharin.";  
 RL Structure 2:7-16(1994).

[5] RN RP X-RAY CRYSTALLOGRAPHY (2.16 ANGSTROMS).  
 RX MEDLINE=91192822; PubMed=814369;  
 RA Rusain J., Tickle I.J., Wood S.P.;  
 RT "Crystal structure of monordin, a type I ribosome inactivating  
 protein from the seeds of Momordica charantia.";  
 RL FEBS Lett. 342:154-158 (1994).

[6] RN RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
 RX MEDLINE=93344383; PubMed=619070;  
 RA Huang Q., Liu S., Tang Y., Jin S., Wang Y.;  
 RT "Studies on crystal structures, active-centre geometry and  
 depurinating mechanism of two ribosome-inactivating proteins.";  
 RL Biochem. J. 309:285-298 (1995).

CC -I-CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one  
 CC specific adenosine on the 28S rRNA.  
 CC -SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 CC -TYPE 1 RIP SUBFAMILY.

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CC EMBL: X57682; CAA40869.1; -.  
 DR DIR: S14273; RLPGCG.  
 DR PDB: 1AHA; 22-JUN-94.  
 DR PDB: 1AHA; 22-JUN-94.

DR PDB: 1AHC; 22-JUN-94.  
 DR PDB: 1MOM; 31-MAY-94.  
 DR PDB; INRG; 07-FEB-95.  
 DR PDB; INRH; 07-FEB-95.  
 DR PDB; INRI; 07-FEB-95.  
 DR PDB; 1P8Q; 21-NOV-94.  
 DR GlycoSuiteDB; P1094; -.  
 DR InterPro; IPR001574; RIP.  
 DR Pfam; PF00161; RIP; 1.  
 DR PRINTS; PR00396; SHIGERICIN.  
 DR PROSITE; PS00275; SHIGA\_RICIN; 1.  
 KW Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin; Signal;  
 KW GLycoprotein; 3D-structure.  
 RN SIGNAL 1 23 RIBOSOME-INACTIVATING PROTEIN MOMORDIN I.  
 KW MISSING IN MATURE PROTEIN.  
 FT SIGNAL 1 23 GLCNAC. . . . .  
 FT STRAND 25 28 GLCOPROTEIN /FTId=CAR\_0000082.  
 FT CHAIN 24 269 N-LINKED (GLCNAC. . . . .  
 FT PROPEP 270 286 CARBOHYD 250 250 /FTId=CAR\_0000082.  
 FT ACT STATE 183 183  
 FT CARBOHYD 70 76  
 FT STRAND 78 79  
 FT TURN 82 88  
 FT STRAND 89 92  
 FT TURN 93 99  
 FT STRAND 99 101  
 FT TURN 100 101  
 FT STRAND 102 105  
 FT HELIX 109 114  
 FT TURN 115 117  
 FT STRAND 124 127  
 FT TURN 120 121  
 FT HELIX 134 141  
 FT STRAND 145 150  
 FT HELIX 152 162  
 FT TURN 163 163  
 FT HELIX 167 186  
 FT STRAND 187 187  
 FT HELIX 188 195  
 FT TURN 196 197  
 FT STRAND 202 202  
 FT HELIX 206 225  
 FT TURN 226 230  
 FT STRAND 231 238  
 FT HELIX 266 263  
 SQ SEQUENCE 286 AA; 31532 MW; E1B013ABBC216CF CRC64;  
 Query Match 28.3%; Score 273; DB 1; Length 286;  
 Best Local Similarity 34.8%; Pred. No. 4-3e-18;  
 Matches 63; Conservative 40; Mismatches 62; Indels 16; Gaps 4;

OY 9 INFITAGATVOSYTNTFRVGRGTVLPNRYGLPI-----NQFILVELSNHAEVSYT 61  
 DB 25 VSFRLSGADPSYGMETKDLRNALPERKEVYNIPLLPSVGAGYLMLHFNQDKIT 84  
 OY 62 LALDDVNAVVGYRAGNSAYFFHPDQDE-AITHLFTDVQNYRTFAFGGNYDLEQLA 120  
 DB 85 VAVDTVNVYINGLLADTSIFF--NEPARAELASQVFRARRKLTPYSSNEYERQIAA 141  
 OY 121 GNLRNENIELNGNPLBEAISALYYSTGGTQLPTLARSFICTIONMISEAARQYIEBEMRT 180

Sun Feb 15 07:30:05 2004

us-10-083-336a-8.rsp

Page 14

Db 142 GKPREKIPIGLPALDSAIStLHYD-----TAAGALLYLIQTTAAARPKYIEQQIQE 196  
Qy 181 R 181  
|  
Db 197 R 197

Search completed: February 10, 2004, 16:23:25  
Job time : 7.27131 secs

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## OM protein - protein search, using sw model

Run on: February 10, 2004, 16:17:00 ; Search time 25.0852 Seconds  
(without alignments)  
1933.961 Million cell updates/sec

Title: US-10-083-336A-8  
Perfect score: 965  
Sequence: 1 MVPKQYPIINFTAGATVQS.....ARFQYTGEMRTRIYRNRRS 188

Scoring table: BLOSUM62  
Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Database : SPTRIMBL23:<sup>\*</sup>

- 1: sp\_archea:<sup>\*</sup>
- 2: sp\_bacteria:<sup>\*</sup>
- 3: sp\_fungi:<sup>\*</sup>
- 4: sp\_human:<sup>\*</sup>
- 5: sp\_invertebrate:<sup>\*</sup>
- 6: sp\_mammal:<sup>\*</sup>
- 7: sp\_mhc:<sup>\*</sup>
- 8: sp\_organelle:<sup>\*</sup>
- 9: sp\_phage:<sup>\*</sup>
- 10: sp\_plant:<sup>\*</sup>
- 11: sp\_rabbit:<sup>\*</sup>
- 12: sp\_virus:<sup>\*</sup>
- 13: sp\_vertebrate:<sup>\*</sup>
- 14: sp\_unclassified:<sup>\*</sup>
- 15: sp\_xvirus:<sup>\*</sup>
- 16: sp\_bacteriaph:<sup>\*</sup>
- 17: sp\_archaea:<sup>\*</sup>

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No. Score Query Match Length DB ID Description

Result No.	Score	Query	Match	Length	DB ID	Description
1	941.7	941.7 ricinus com	941.7	541	10	041174
2	374.5	38.8	580	10	094Bw3	Q9abw3 cinnamomum
3	372.5	38.6	580	10	094Bw4	Q9abw4 cinnamomum
4	370.5	38.4	581	10	094Bw5	Q9abw5 cinnamomum
5	368.5	38.2	549	10	09FV22	Q9fV22 cinnamomum
6	334	34.6	289	10	094KE4	Q94KE4 trichosanth
7	332	34.4	289	10	041216	Q41216 trichosanth
8	329.5	34.1	563	10	004367	Q04367 sambucus ni
9	326	33.8	247	10	09LRE3	Q9LRE3 trichosanth
10	323.5	33.5	564	10	09AVR2	Q9avr2 sambucus eb
11	318.5	33.0	528	10	006076	Q06076 sambucus preca
12	317	32.8	270	10	08LPV7	Q8LPV7 trichosanth
13	310.5	32.2	252	10	038761	Q38761 abrus preca
14	307.5	31.9	563	10	094582	Q94582 sambucus ni
15	307.5	31.9	563	10	08GT32	Q8gt32 sambucus ni
16	311.6	31.6	270	10	041611	Q41611 trichosanth

ALIGNMENTS					
<b>RESULT 1</b>					
ID	Q41174	PRELIMINARY;	PRT;	541 AA.	
AC	Q41174				
DT	01-NOV-1996 (TREMBLref. 01; Created)				
DT	01-NOV-1996 (TREMBLref. 01; Last sequence update)				
DT	01-MAR-2003 (TREMBLref. 23; Last annotation update)				
DE	Pro ricin A chain (EC 3.2.2.22) (rRNA N-glycosidase)				
DB	(Fragment).				
OS	Ricinus communis (Castor bean).				
OC	Buxtoraceae; Viridiplantae; Streptophytina; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; eu dicots; core eudicots; Rosidae;				
OC	eurosid I; Malpighiales; Euphorbiaceae; Ricinaceae;				
OX	[1] _TaxID=3988;				
RN	SEQUENCE FROM N. A.				
RP	MEDLINE=22338377; PubMed=1633311;				
RA	Roberts L.M.; Tregeair J.W.; Lord J.M.;				
RT	"Molecular cloning of ricin,";				
RL	Targeted Diagn. Ther. 7:81-97 (1992).				
CC	-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 2BS RNA.				
CC	-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.				
EMBL	SA0366; AAB22582.1; -.				
DR	HSSP; P02879; IBR6.				
DR	"Molecular cloning of ricin."				
DR	InterPro; IPR000772; Ricin_B_lectin.				
DR	InterPro; IPR001574; RIP.				
DR	InterPro; IPR001400; Somatotropin.				
DR	Pfam; PF00652; Ricin_B_lectin; 6.				
DR	Pfam; PF00161; RIP; I_				
DR	PRINTS; PR00596; SHIGARICIN.				
DR	SMART; SM00458; RICIN; 2.				
DR	PROSITE; PS50231; RICIN_B_LECTIN; 2.				
DR	PROSITE; PS00275; SHIGA_RICIN; 1.				
DR	PROSITE; PS00338; SOMATOTROPIN_-; 1.				
KW	Hydrolase; Toxin.				
FT	NON_TER	1	1		
SEQ	SEQUENCE	541 AA;	60281 MW;	2B7B2CDF1F2E9D9 CRC64;	

Query Match	97.5%	Score 941;	DB 10;	Length 541;	
Best Local Similarity	94.9%	Pred. No. 2-4e-81;			
Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;					
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53 SNHAELSVTLALDVTNAITYGYRAGNSAYFFHDNQEDAATIHLFLDVQNTTFAFGGN 112					
53 SNHAELSVTLALDVTNAITYGYRAGNSAYFFHDNQEDAATIHLFLDVQNTTFAFGGN 122					
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113 YDRLEQLAGLRENIELNGNPLEEASALYYSTGGTQLPTLARSFIICQMISEAARFQ 172					
123 YDRLEQLAGLRENIELNGNPLEEASALYYSTGGTQLPTLARSFIICQMISEAARFQ 182					
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173 YIEGMRTRIYRNRS 188					
183 YIEGMRTRIYRNRS 198					
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RESULT 3					
094BWS					
ID Q94BWS4; PRELIMINARY; PRT; 580 AA.					
AC Q94BWS4; PRELIMINARY; PRT; 580 AA.					
DT 01-DEC-2001 (TREMBLrel. 19, Created)					
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)					
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)					
DE Type 2 ribosome-inactivating protein cinnamomin II precursor					
DE (BC 3-2-22) (rRNA N-glycosidase).					
OS Cinnamomum camphora (Camphor tree).					
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;					
OC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.					
NCBI_TaxID:13429; [1]					
RN [1] - TaxID:13429;					
RP SEQUENCE FROM N.A.					
RA Yang Q.; Gong Z.Z.; Liu W.Y.;					
RT "Molecular cloning of three type 2 RIP (ribosome-inactivating protein genes encoding cinnamomin proteins and study of their expression patterns";					
RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.					
RT -!- CATALYTIC ACTIVITY: ENDONUCLEASE: N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE IN THE 28S RNA.					
RT -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.					
DR EMBL; AY039802; AAC82459; 1; -					
DR InterPro; IPR000772; Ricin_B_lectin.					
DR InterPro; IPR001574; RIP.					
PFam; PF00652; Ricin_B_lectin; 6.					
DR Pfam; PF00162; RIP; 1.					
PRINTS; PR00396; SHIGARICIN.					
DR SMART; SM00455; Ricin; 2.					
DR PROSITE; PS50331; Ricin_B_LECTIN; 2.					
KW Hydrolase; Signal; Toxin.					
FT SIGNAL [1] 32 POTENTIAL.					
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Query Match 6 YPIINFTAGATVQSYTNFTRAVGRGTTGAGNSAYFFHDNQEDAATIHLFLDVQNTTFAFGGNPI-----NQEFILVLSN-H 55					
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Matches 89; Conservative 27; N mismatches 56; Indels 15; Gaps 5;					
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33 YQTWTFITTRNATKTSYQFTEALRQLASSEPHGTPVNRDGSTVPSKRFILVLSNWA 92					
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56 AEIYSTLALDYTNAYVGTAQNSAYFFHDNQEDAATIHLFLDVQNTTFAFGGNPI-----NQEFILVLSN-H 55					
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56 AEILAGNLIRENIELNGNPLEEAISALYYSTGGTQLPTLARSFIICQMISEAARFQYE 175					
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Best Local Similarity 38.8%; Score 374.5%; DB 10; Length 580;					
Matches 90; Conservative 26; N mismatches 56; Indels 15; Gaps 5;					
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56 AEIAGNLIRENIELNGNPLEEAISALYYSTGGTQLPTLARSFIICQMISEAARFQYE 115					
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AC Q94BWS5; PRELIMINARY; PRT; 581 AA.					
DT 01-DEC-2001 (TREMBLrel. 19, Created)					
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)					
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)					
DE Type 2 ribosome-inactivating protein cinnamomin I precursor					
DE (BC 3-2-22) (rRNA N-glycosidase).					
PRINTS; PR00396; SHIGARICIN.					
DR SMART; SM00458; Ricin; 2.					
DR PROSITE; PS50231; Ricin_B_LECTIN; 2.					
KW Hydrolase; Signal; Toxin.					
FT SIGNAL [1] 32 POTENTIAL.					
FT CHAIN 33 580 TYPE 2 RIBOSOME-INACTIVATING PROTEIN CINNAMOMIN III.					
FT SEQ 580 AA; 64265 MW; 3784289EC0E0CBFF CRC64;					
Query Match 116 LEQLAGNLIRENIELNGNPLEEAISALYYSTGGTQLPTLARSFIICQMISEAARFQYE 175					
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DT 01-DEC-2001 (TREMBLrel. 19, Created)					
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DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)					
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DR SMART; SM00458; Ricin; 2.					
DR PROSITE; PS50231; Ricin_B_LECTIN; 2.					
KW Hydrolase; Signal; Toxin.					
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DT 01-DEC-2001 (TREMBLrel. 19, Created)					
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)					
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)					
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DE (BC 3-2-22) (rRNA N-glycosidase).					
PRINTS; PR00396; SHIGARICIN.					
DR SMART; SM00458; Ricin; 2.					
DR PROSITE; PS50231; Ricin_B_LECTIN; 2.					
KW Hydrolase; Signal; Toxin.					
FT SIGNAL [1] 32 POTENTIAL.					
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DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)					
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)					
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PRINTS; PR00396; SHIGARICIN.					
DR SMART; SM00458; Ricin; 2.					
DR PROSITE; PS50231; Ricin_B_LECTIN; 2.					
KW Hydrolase; Signal; Toxin.					
FT SIGNAL [1] 32 POTENTIAL.					
FT CHAIN 33 580 TYPE 2 RIBOSOME-INACTIVATING PROTEIN CINNAMOMIN III.					
FT SEQ 580 AA; 64265 MW; 3784289EC0E0CBFF CRC64;					
Query Match 116 LEQLAGNLIRENIELNGNPLEEAISALYYSTGGTQLPTLARSFIICQMISEAARFQYE 175					
Best Local Similarity 38.8%; Score 374.5%; DB 10; Length 580;					
Matches 90; Conservative 26; N mismatches 56; Indels 15; Gaps 5;					
/					
33 YQTWTFITTRNATKTSYQFTEALRQLASSEPHGTPVNRDGSTVPSKRFILVLSNWA 92					
/					
56 AEIAGNLIRENIELNGNPLEEAISALYYSTGGTQLPTLARSFIICQMISEAARFQYE 115					
/					
AC Q94BWS9; PRELIMINARY; PRT; 581 AA.					
DT 01-DEC-2001 (TREMBLrel. 19, Created)					
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)					
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)					
DE Type 2 ribosome-inactivating protein cinnamomin I precursor					
DE (BC 3-2-22) (rRNA N-glycosidase).					
PRINTS; PR00396; SHIGARICIN.					
DR SMART; SM00458; Ricin; 2.					
DR PROSITE; PS50231; Ricin_B_LECTIN; 2.					
KW Hydrolase; Signal; Toxin.					
FT SIGNAL [1] 32 POTENTIAL.					
FT CHAIN 33 580 TYPE 2 RIBOSOME-INACTIVATING PROTEIN CINNAMOMIN III.					
FT SEQ 580 AA; 64265 MW; 3784289EC0E0CBFF CRC64;					
Query Match 116 LEQLAGNLIRENIELNGNPLEEAISALYYSTGGTQLPTLARSFIICQMISEAARFQYE 175					
Best Local Similarity 38.8%; Score 374.5%; DB 10; Length 580;					
Matches 90; Conservative 26; N mismatches 56; Indels 15; Gaps 5;					
/					
33 YQTWTFITTRNATKTSYQFTEALRQLASSEPHGTPVNRDGSTVPSKRFILVLSNWA 92					
/					
56 AEIAGNLIRENIELNGNPLEEAISALYYSTGGTQLPTLARSFIICQMISEAARFQYE 115					
/					
AC Q94BWS10; PRELIMINARY; PRT; 581 AA.					
DT 01-DEC-2001 (TREMBLrel. 19, Created)					
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)					
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)					
DE Type 2 ribosome-inactivating protein cinnamomin I precursor					
DE (BC 3-2-22) (rRNA N-glycosidase).					
PRINTS; PR00396; SHIGARICIN.					
DR SMART; SM00458; Ricin; 2.					
DR PROSITE; PS50231; Ricin_B_LECTIN; 2.					
KW Hydrolase; Signal; Toxin.					
FT SIGNAL [1] 32 POTENTIAL.					
FT CHAIN 33 580 TYPE 2 RIBOSOME-INACTIVATING PROTEIN CINNAMOMIN III.					
FT SEQ 580 AA; 64265 MW; 3784289EC0E0CBFF CRC64;					
Query Match 116 LEQLAGNLIRENIELNGNPLEEAISALYYSTGGTQLPTLARSFIICQMISEAARFQYE 175					
Best Local Similarity 38.8%; Score 374.5%; DB 10; Length 580;					
Matches 90; Conservative 26; N mismatches 56; Indels 15; Gaps 5;					
/					
33 YQTWTFITTRNATKTSYQFTEALRQLASSEPHGTPVNRDGSTVPSKRFILVLSNWA 92					
/					
56 AEIAGNLIRENIELNGNPLEEAISALYYSTGGTQLPTLARSFIICQMISEAARFQYE 115					
/					
AC Q94BWS11; PRELIMINARY; PRT; 581 AA.					
DT 01-DEC-2001 (TREMBLrel. 19, Created)					
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)					
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)					
DE Type 2 ribosome-inactivating protein cinnamomin I precursor					
DE (BC 3-2-22) (rRNA N-glycosidase).					
PRINTS; PR00396; SHIGARICIN.					
DR SMART; SM00458; Ricin; 2.					
DR PROSITE; PS50231; Ricin_B_LECTIN; 2.					
KW Hydrolase; Signal; Toxin.					
FT SIGNAL [1] 32 POTENTIAL.					
FT CHAIN 33 580 TYPE 2 RIBOSOME-INACTIVATING PROTEIN CINNAMOMIN III.					
FT SEQ 580 AA; 64265 MW; 3784289EC0E0CBFF CRC64;					
Query Match 116 LEQLAGNLIRENIELNGNPLEEAISALYYSTGGTQLPTLARSFIICQMISEAARFQYE 175					
Best Local Similarity 38.8%; Score 374.5%; DB 10; Length 580;					
Matches 90; Conservative 26; N mismatches 56; Indels 15; Gaps 5;					
/					
33 YQTWTFITTRNATKTSYQFTEALRQLASSEPHGTPVNRDGSTVPSKRFILVLSNWA 92					
/					
56 AEIAGNLIRENIELNGNPLEEAISALYYSTGGTQLPTLARSFIICQMISEAARFQYE 115					
/					
AC Q94BWS12; PRELIMINARY; PRT; 581 AA.					
DT 01-DEC-2001 (TREMBLrel. 19, Created)					
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)					
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)					
DE Type 2 ribosome-inactivating protein cinnamomin I precursor					
DE (BC 3-2-22) (rRNA N-glycosidase).					
PRINTS; PR00396; SHIGARICIN.					
DR SMART; SM00458; Ricin; 2.					
DR PROSITE; PS50231; Ricin_B_LECTIN; 2.					
KW Hydrolase; Signal; Toxin.					
FT SIGNAL [1] 32 POTENTIAL.					
FT CHAIN 33 580 TYPE 2 RIBOSOME-INACTIVATING PROTEIN CINNAMOMIN III.					
FT SEQ 580 AA; 64265 MW; 3784289EC0E0CBFF CRC64;					
Query Match 116 LEQLAGNLIRENIELNGNPLEEAISALYYSTGGTQLPTLARSFIICQMISEAARFQYE 175					
Best Local Similarity 38.8%; Score 374.5%; DB 10; Length 580;					
Matches 90; Conservative 26; N mismatches 56; Indels 15; Gaps 5;					
/					
33 YQTWTFITTRNATKTSYQFTEALRQLASSEPHGTPVNRDGSTVPSKRFILVLSNWA 92</td					

OS Cinnamomum camphora (Camphor tree). OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; OC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum. OX NCBI_TAXID=13429; RN [1] RP SEQUENCE FROM N.A. RA Yang Q., Gong Z.Z., Liu W.Y.; RA "Molecular cloning of three type 2 RIP (ribosome-inactivating protein patterns); Genes encoding cinnamomin proteins and study of their expression patterns." Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.	DR InterPro; IPR000772; Ricin_B_lectin. DR InterPro; IPR001574; RIP. DR Pfam; PF00651; Ricin_B_lectin; 5. DR Pfam; PF00161; RIP; 1. PRINTS; PR00396; SHIGARICIN. SMART; SM00458; RICIN; 2. PROSITE; PS50231; RICIN_B_LECTIN; 2. KW Hydrolase; Toxin. FT NTER 1 FT SEQ 549 AA; 60648 MW; 026078E607CA44B0 CRC64;
CC !- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RNA. CC !- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.	Query Match 38.2%; Score 368.5; DB 10; Length 549; Best Local Similarity 48.1%; Pred. No. 1..3e-26; Matches 90; Conservative 25; Mismatches 57; Indels 15; Gaps 5;
DR EMBL:AY039801; AAK8245B1; - DR InterPro; IPR0001574; RIP. DR Pfam; PF00652; Ricin_B_lectin; 5. DR Pfam; PF00161; RIP; 1. SMART; SM00458; SHIGARICIN. DR PROSITE; PS50231; RICIN_B_LECTIN; 2. DR Hydrolase; Signal; Toxin. KW Hydrolase; Signal; Toxin. FT SIGNAL 1 32 FT CHAIN 33 591 TYPE 2 RIBOSOME-INACTIVATING PROTEIN SQ SEQUENCE 581 AA; 64215 MW; 638F5FB8FBA3D196 CRC64;	QY 6 YPIINFATTAGTVOSYTNFIRAVGRLT-----VLPNRGLPINORFILVELSN-H 55 Best Local Similarity 38.4%; Score 370.5; DB 10; Length 581; Matches 90; Conservative 25; Mismatches 57; Indels 15; Gaps 5; Result 6 QY 6 YPIINFATTAGTVOSYTNFIRAVGRLT-----VLPNRGLPINORFILVELSN-H 55 Db 33 YQTWFTTQNATKTSYTFQFLERALQALASEEPHGPVRERSVPDSKRFLVELSNWA 92 PRELIMINARY; PRT; 289 AA. QY 56 AELSTYTLAIDVNTNAYVGYRAGNSAYFEHDNOEAEATHLFDTDVQRYTFAFGGNYR 115 Db 93 ADSPTVLAIDVNTNAYVATRGSQFFERGNDP-PALENNLLPDTK-RYTFPPSGSTD 149 QY 116 LEQLAGNLRENIELGNGPLLEAISALYYYSTGGTOLPTLARSFICIONISEARFOYIE 175 Db 150 LEGYAGERREBELLGMDDPLENAISALWISNL--NQRLALARSLIVVOMVAEVRFETIE 207 QY 176 GEMTRI 182 Db 208 YRVRSI 182 Result 5 ID Q9FV72 PRELIMINARY; PRT; 549 AA.
RN	SEQUENCE FROM N.A. RA Yuan H., Wang L., Wang Y., An C., Chen Z.; RA Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases. CC !- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RNA. CC !- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. CC !- SIMILARITY: BELONGS TO THE 28S RNA. DR EMBL: AF367252; AAC52901; -. Last sequence update) DR InterPro; IPR001574; RIP. DR Pfam; PF00161; RIP; 1. PRINTS; PR00396; SHIGARICIN. SMART; SM00458; RICIN; 1. DR PROSITE; PS00275; SHIGA_RICIN; 1. KW Hydrolase; Signal; Toxin. FT SIGNAL 1 23 POTENTIAL. FT CHAIN 24 270 TRICHOSANTHIN. SQ SEQUENCE 289 AA; 31706 MW; A6D5602549CA5657 CRC64;
RP SEQUENCE FROM N.A. RA Xie L., Liu W.-Y., Wang F.-D.; RT "Molecular cloning of cinnamomin A-, B-chain and the expression, purification, characterization and mutagenesis of the A-Chain."; RT Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases. RL !- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RNA. CC !- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. DR EMBL: AF29548; AAF68978..2; -. Last sequence update) DR HSSP; P02879; ZAAI.	Query Match 34.6%; Score 334; DB 10; Length 289; Best Local Similarity 38.9%; Pred. No. 1e-23; Matches 72; Conservative 42; Mismatches 49; Indels 22; Gaps 5;
RN	QY 9 INFITAGATVOSYTNFIRAVGRLT-----VLPNRGLPINORFILVELSNWAEL 58 Db 25 VSFRLSGATSSSSYGVFISNLR--KALPNERKLDPPLRSIISPGSQRVALIHLTYADE 81 QY 59 SVTLADVNAYVVGYRAGNSAYFFHPRNQEDA-EAITHLFTDVQRYTFAFGGNYDLE 117



-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPeCIFIC ADENOSINE ON THE 2'8S RNA.

CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.

DR ENMBL: AB039224; BAA925301; -.

DR INSSP; P09989; IMRJ.

DR InterPro; IPR01574; RIP.

DR PFAM; PF00161; RIP; 1.

DR PRINTS; PR00396; SHIGARICIN.

DR PROSITE; PS50231; SHIGA\_RICIN; 1.

KW Hydrolase; Toxin.

FT NON\_TER 1

FT NON\_TER 247 247

SQ SEQUENCE 247 AA; 27199 MW; 89811AC32B92F03F CRC64;

Query Match Score 32.5%; DB 10; Length 564;

Best Local Similarity 40.0%; Pred. No. 2.6e-22;

Matches 76; Conservative 38; Mismatches 51; Indels 25; Gaps 6;

Qy 6 YPIINFATAGATVQSNTNFIRAVRGR-----LTVLPRVGQLPNQRFILVELSNH 55

Db 28 IPSVSTNAGKSTTRFLANLRDFTATGYEYNGPLVERRESEYQVNRFVLRVITY 87

Qy 56 AELSYTTLADVTNAYVYVGYRAGNSAYFFHPDQNQDEAEAI--THLFDTDVQNYTEAFGQY 113

Db 88 NGDTVTSAVDVNLVLYAFSANGNSTEF----KDATELQSNLFGT-TOTLTSFGNY 141

Qy 9 INFATAGATVQSNTNFIRAVR-----GRLTVP-NRVLGLPINQRFLVLSNHAEELSVT 61

Best Local Similarity 33.8%; Pred. No. 4.9e-23;

Matches 72; Conservative 44; Mismatches 50; Indels 16; Gaps 5;

Db 2 VSPFLSGCTSSSTCVFISMRKALPYKXIDPFLRSTLPGSORYAIIHNTYADETIS 61

Qy 62 LADYTNNAYVYVGYRAGNSAYFFHPDQNQDEA-EATHLFTDVQNYTEAFGQYDRLEQIA 120

Db 62 VAIDVTNVTYVMGTRAGDISYF--NEASATEAKYVFKDARKVTLYSGNVERLQIAA 118

Qy 121 GNLPIENTLGNGPLFEEAISALYYGSTGGTQLPLTARSEFICIQMISEARFYLEGEMRT 180

Db 119 GKTCRNTIPLGLPAQLSDATTLYFTYNNAN---SAASALMVLIQSTSEARYKTFEOQIGK 173

Qy 181 RI 182

Db 174 RV 175

RESULT 10

Q9AVR2 PRELIMINARY; PRT; 564 AA.

ID Q9AVR2 PRELIMINARY; PRT; 564 AA.

AC O9AVR2; 1

DT 01-JUN-2001 (TREMBLrel. 17, Created)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE Ribosome-inactivating protein precursor (EC 3.2.2.22) (rRNA

GN RN

OS Sambucus ebulus

OC Sambidaplantes; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eu dicotyledons; core eudicots;

OC Asteridae; campanulids; Dipsacales; Adoxaceae; Sambucus.

OX NCBI\_TaxID=28503;

RP SEQUENCE FROM N.A.

RC TISSUE=leaf;

RA Gibres T., Iglesias R., Perez Y., Ferreras J.M., Cidores L.;

RT "Molecular cloning of ebulin L".

RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.

CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RNA.

CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.

DR ENMBL; AU740822; CAC33178.1; -.

DR HSSP; P02879; 2AAI.

DR InterPro; IPR000772; Ricin\_B\_lectin.

DR InterPro; IPR001574; Ricin\_B\_lectin.

DR Pfam; PF00161; RIP; 1.

DR PRINTS; PR00396; SHIGARICIN.

DR SMART; SM00458; RICIN\_BLECTIN; 2.

DR PROSITE; PS50231; RICIN\_B\_LECTIN; 1.

KW Glycosidase; Hydrolase; Signal; Toxin.

FT SIGNAL 1 25

FT CHAIN 26 298

FT CHAIN 299 564

DR PROSITE; PS50231; RICIN\_B\_LECTIN; 2.

DR PROSITE; PS00275; SHIGA\_RICIN; 1.

DR PROSITE; PS50231; RICIN\_B\_LECTIN; 2.

DR PROSITE; PS00275; SHIGA\_RICIN; 1.

FT CHAIN 1 25

FT CHAIN 26 298

FT CHAIN 299 564

SQ SEQUENCE 564 AA; 62694 MW; 8261681A6DB55CB8 CRC64;

Query Match Score 33.5%; DB 10; Length 564;

Best Local Similarity 43.3%; Pred. No. 7.2e-22;

Matches 81; Conservative 22; Mismatches 69; Indels 15; Gaps 4;

Qy 5 QYPININFATAGATVQSNTNFIRAVRGR-----VLPNVGLPQNQRFILVELSNH 56

Db 1 QDQVIKFITEGATQSQYQFIEALRQITGGLIHDIPVLPDPFTVEENRYTVELSNH 60

Query Match Score 31.85%; DB 10; Length 528;

Best Local Similarity 43.3%; Pred. No. 7.2e-22;

Matches 81; Conservative 22; Mismatches 69; Indels 15; Gaps 4;

Qy 57 ELSVTLADVTNAYVYVGYRAGNSAYFFPDQNQDEAEAI--THLFDTDVQNYTEAFGQY 116

Db 61 RESIEVGIDVTNAYVYVGASOYFL--RDAPASASTYLFGTQ-RYSLREDGSYQDL 116

Qy 117 EOLAGNIRENTLNGPLEEALISALLYSTGGTQLPPTLARSFICTIONIMISEAARFOYIEG 176  
 DB 117 ERWAHOTREEISLGLOALTHAIS---FLRGASNDEEKARTLIVIOMASSAARYRCISN 173  
 Qy 177 EMRTRTR 183  
 DB 174 RVGVSIR 180

RESULT 12  
 Q8LPV7 PRELIMINARY; PRT; 270 AA.  
 ID Q8LPV7;  
 AC (TREMBLrel. 22, Created)  
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Trichosanthin precursor (EC 3.2.2.22) (rRNA N-glycosidase)  
 DE (Fragment).  
 GN TCS.  
 OS Trichosanthes kirilowii (Mongolian snake-gourd).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids I; Fabales; Fabaceas; Papilionoideae; Abreuae; Abrus.  
 NCBI\_TAXID=3816;  
 RN [1]  
 RP TISSUE=N.A.  
 RC TISSUE=LIAF;  
 RX MEDLINE=91201129; PubMed=2016300;  
 RA Evensen G., Mathiesen A., Sundan A.;  
 RT "Direct molecular cloning and expression of two distinct abrin A-chains", J. Biol. Chem. 266:848-852 (1991).  
 RL J. Biol. Chem. 266:848-852 (1991).  
 CC -!- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RNA.  
 CC -!- ABRINA-A IS MORE TOXIC THAN RICIN.  
 CC -!- FUNCTION: THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT FACILITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT PRECEDES ENDOCYTOSIS.  
 CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RNA.  
 CC -!- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.  
 CC -!- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).  
 CC -!- SIMILARITY: TO OTHER BACTERIAL AND PLANTS RIBOSOME-INACTIVATING PROTEINS BELONGS TO TYPE 2 RIP.  
 DR EMBL; X54872; CA38654.; -.  
 DR HSSP; P11140; LABR.  
 DR InterPro; IPR01574; RIP.  
 DR Pfam; PF00161; RIP; 1.  
 DR PRINTS; PR00396; SHIGARICIN.  
 DR PROSITE; PS00274; SHIGA\_RICIN; 1.  
 DR Hydrolase; Glycosidase; Toxin; Repeat; Glycoprotein; Lectin.  
 DR CHAIN 1 252 252  
 FT NON\_TER 252 252  
 SQ SEQUENCE 252 AA; 28309 MW; BBFC846B9E9225DE CRC64;

Query Match 32.2%: Score 310.5; DB 10; Length 252;  
 Best Local Similarity 43.2%; Pred. No. 1.5e-21;  
 Matches 79; Conservative 22; Mismatches 67; Indels 15; Gaps 4;

Qy 9 INFETTAGATVOSYTNTFRAYVRGRL-----TVLPNRVGLPINFQFLVLSNHAEHSV 60  
 DB 6 IKFSTCATOSYKOPTEAERLRRGGLHDIPVLRDPPTVEERYITYELNSNRESI 65

Qy 9 INFETTAGATVOSYTNTFRAYVRGRL-----TVLPNRVGLPINFQFLVLSNHAEHSV 60  
 DB 6 IKFSTCATOSYKOPTEAERLRRGGLHDIPVLRDPPTVEERYITYELNSNRESI 65

Qy 61 TIALDTDTNATVYGYRAGNSAYFFPDNQEDA-EAITHIFTDVQNYTFAGFGNYDRLEOLA 120  
 DB 66 EVGIDVTNTAVYAYRGSQSYSTFL--RDAPASASTYLFTGTQ-RYSLRFDSYQGLERWVA 121

Qy 121 GNLRNENELGNGPLEAISALYYSTGGTQLPQLPTLARSFICTIONIMISEAARFOYIEGMR 180  
 DB 122 HOTREQLSGLQALTAIS--FLRGASNDEEKARTLIVIOMASEAARYRISNRGV 178

Qy 181 RIR 183  
 DB 179 SIR 181

RESULT 14  
 Q845S2 PRELIMINARY; PRT; 563 AA.  
 ID Q945S2;  
 AC Q945S2;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Ribosome-inactivating protein (EC 3.2.2.22) (rRNA AVL).  
 GN Sambucus nigra (European elder).  
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; campanulids; Dipsacales; Adoxaceae; Sambucus.  
 RI RIP.

RESULT 13  
 Q38760 PRELIMINARY; PRT; 252 AA.  
 ID Q38760;  
 AC Q38760;  
 DT 01-NOV-1998 (TREMBLrel. 08, Created)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Abrin-E (rRNA N-glycosidase) (EC 3.2.2.22) (Fragment).

OX NCBI\_TaxID=4202;  
 RN [1] SEQUENCE FROM N.A.  
 RC TISSUE=Leaf;  
 RA "Van Damme E.J.M.;  
 RT "Characterization and cloning of lectins and ribosome-inactivating  
 proteins from Sambucus nigra leaves.";  
 RT Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 CC "-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
 SPECIFIC ADENOSINE ON THE 28S RNA.  
 CC "-!- SIMILARITY: TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 DR EMBL; ARA0135; AAL04123.1;  
 DR InterPro; IPR001572; Ricin\_B\_lectin.  
 DR Pfam; PF00652; Ricin\_B\_lectin; 6.  
 DR Pfam; PF00161; RIP; 1.  
 DR PRINTS; PR00336; SHIGARICIN.  
 DR SMART; SM00458; RICIN.  
 DR PROSITE; PS50231; RICIN\_B\_LECTIN; 2.  
 DR PROSITE; PS00275; RICINA\_RICIN; 1.  
 KW Hydrolase; Toxin.  
 SQ SEQUENCE 563 AA; 62242 MW; 07F7CBEDCF33BF10 CRC64;  
 Query Match Score 307.5; DB 10; Length 563;  
 Best Local Similarity 38.4%; Pred. No. 8.9e-21;  
 Matches 73; Conservative 36; Mismatches 56; Indels 25; Gaps 5;  
 QY 6 YPLINFTTAGATVQSYTNEFIRAVR-----GRITVLPNRGLPTNQRFLVELSNH 55  
 DB 28 YPSVSEFNLDKASATYRDPFLSNLRKTVAATGYEVNGLPVTRERESEVOVKSFRFLVPLNY 87  
 QY 56 AELSTYLALDVNTAYVGVRAGNSAYFFHDQNQDAEAI--THLFTDVONRYTFAGGNY 113  
 DB 88 NGNTVTLAVNTNLVYVAFGANSYFF----KDATEQKSNLFVGTCN-TLSFTGNY 141  
 QY 114 DRLEOLAGNRENTLGNGPYLEAALSALVYYSTGGTQLPLTARSFIICQMSSEAARFOY 173  
 DB 142 DNLETAANTRRESTELGPSPLDGATSLVHG-----SVARSLVVYQMVSEAARFRY 194  
 QY 174 IEGEMRTRIR 183  
 DB 195 IEQEVRRSLQ 204

Search completed: February 10, 2004, 16:26:38  
 Job time : 25.0852 secs

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RESUTR 15

Q8GT32 PRELIMINARY; PRT; 563 AA.  
 ID Q8GT32; PRELIMINARY;  
 AC Q8GT32; PRELIMINARY;  
 DT 01-MAR-2003 (TREMBL); 23, Created)  
 DT 01-MAR-2003 (TREMBL); 23, Last sequence update)  
 DT 01-MAR-2003 (TREMBL); 23, Last annotation update)  
 DE (EC 3.2.2.22).  
 OS Sambucus nigra (European elder).  
 OC Spermatophyta; Viridiplantae; Strptophyta; Embryophyta; Tracheophyta;  
 OC Eukaryota; Campanulidae; Asteridae; Dipscales; Aroidaceae; Sambucus.  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; campanulids; Dipscales; Aroidaceae; Sambucus.  
 OX NCBI\_TaxID=4202;  
 RN [1] SEQUENCE FROM N.A.  
 RC TISSUE=Leaf;  
 RA Girbes T.; Arias F.J.; Antolin P.;  
 RT "Characterization and molecular cloning of Nigrin 1, a type two  
 ribosome-inactivating protein from leaves of elder (Sambucus nigra)." ;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF249280; AAN86130.1; -.  
 KW Hydrolase; Glycosidase.  
 SQ SEQUENCE 563 AA; 62173 MW; 0EB236421FC5E04F CRC64;  
 Query Match Score 307.5; DB 10; Length 563;  
 Best Local Similarity 38.4%; Pred. No. 8.9e-21;  
 Matches 73; Conservative 36; Mismatches 56; Indels 25; Gaps 5;

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OM protein - protein search, using sw model

Run on: February 10, 2004, 16:13:20 ; Search time 31:54:19 Seconds  
(without alignments)  
930.966 Million cell updates/sec

Title: US-10-083-336A-9  
Perfect score: 951  
Sequence: 1 IFPKQYPIINFTAGATVQSQ.....ARFQYIEGEMTRIRYNNRS 185

Scoring table: BLOSUM62

Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_19Jun03:\*

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2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the result being printed.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	934.5	98.3	267	14	AAR37290	Ricin A chain.
2	934.5	98.3	267	16	AAR3902	Ricin A-chain (RPA)
3	934.5	98.3	290	18	AAN25136	Ricin A-chain ribo
4	934.5	98.3	290	18	AAN21699	Ricin A-chain RPA.
5	934.5	98.3	332	8	AAP70097	Ricin A. Esteric
6	934.5	98.3	332	8	AAP70838	Sequence of Ricinu
7	934.5	98.3	332	10	AAP56339	Ricin A encoded by Anti-dictaract immu
8	934.5	98.3	554	16	AAR10827	Ricin D. Ricinus
9	934.5	98.3	562	10	AAP90079	

Result No.	Score	Query	Match	Length	DB ID	Description
10	934.5	98.3	565	6	AAP50166	Sequence of prepro
			934.5	98.3	AAG78300	Castor bean prepro
			934.5	98.3	AAG78304	Modified castor bean prepro
			934.5	98.3	AAP70326	Sequence of Ricinu
			934.5	98.3	AAP25787	Castorbean ricin.
			934.5	98.3	AAY55892	Ricinus communis r
			934.5	98.3	AAY78392	Castor bean prepro
			934.5	98.3	AAG78301	Castor bean prepro
			934.5	98.3	AAG78302	Biosynthetic multi
			934.5	98.3	AAP80164	Preproricin.
			934.5	97.7	AAP60240	Sequence of ricin.
			927.5	97.5	AAR39570	Sequence of Ricinu
			927.5	97.5	AAP70325	DNA sequence of ri
			927.5	97.3	AAP94193	Ricin A from PDC1
			924.5	97.2	AAR30722	Ricin A from PDC1
			924.5	97.2	AAB19465	Amino acid sequenc
			924.5	97.2	AAR39571	Sequence of G-RIT.
			923.5	97.1	AAR06554	Ricin A gene produ
			917.5	96.5	AAR74176	Ricin A chain (RTA
			901.5	94.9	AAR32430	Ricin A. Synthetic
			845	88.9	AAW25143	Castor oil Plant a
			845	88.9	AAW21706	R. communis agglic
			803	84.4	AAP70324	Sequence of Ricin
			698	73.4	AAP95648	Ricin agglutinin A
			375	35.5	AAR67359	Trichosanthin anti
			375	35.5	AAR07518	Amino acid sequenc
			375	35.5	AAR25573	Synthetic alpha-tri
			375	35.5	AAR25573	Mature alpha-Trich
			375	35.5	AAR25573	Trichosanthin (a r
			375	35.5	AAW21703	Trichosanthin. Tr
			375	35.5	AAR07514	Trichosanthin from
			375	35.5	AAR25572	Trichosanthin from
			375	35.5	AAR29272	Trichosanthin prot
			375	35.5	AAR32286	Encodes Chinese cu
			375	35.5	AAR55129	Alpha-trichosanthi
			375	35.5	AAW10468	Chinese cucumber a

#### ALIGNMENTS

RESULT 1  
ID AAR37290  
ID AAR37290 standard; protein; 267 AA.

AC AAR37290;

XX XX

DT 25-MAR-2003 (updated)

DR 09-JAN-2003 (updated)

DD 13-SEP-1993 (first entry)

XX XX

DE Ricin A chain.

XX XX

Type II ribosome-inactivating protein; type II RIP; gelonin; toxin.

OS Unidentified.

#### SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	934.5	98.3	267	14	AAR37290	Ricin A chain.
2	934.5	98.3	267	16	AAR3902	Ricin A-chain (RPA)
3	934.5	98.3	290	18	AAN25136	Ricin A-chain ribo
4	934.5	98.3	290	18	AAN21699	Ricin A-chain RPA.
5	934.5	98.3	332	8	AAP70097	Ricin A. Esteric
6	934.5	98.3	332	8	AAP70838	Sequence of Ricinu
7	934.5	98.3	332	10	AAP56339	Ricin A encoded by Anti-dictaract immu
8	934.5	98.3	554	16	AAR10827	Ricin D. Ricinus
9	934.5	98.3	562	10	AAP90079	

PT Analogues of type I ribosome inactivating protein - useful as  
PT cytotoxic agents, immuno toxins for treating auto immune diseases,  
PT cancer, graft versus host disease and selective cell killing in-vivo

Claim 1; Page 92; 163pp; English.

The invention covers analogues of Type I RIPS. Ricin is a Type II RIP whose A chain is homologous to plant type I RIPS. The analogues of the invention have a cysteine available for intermolecular disulphide bonding at an amino acid position corresp. to a position not naturally available for binding; the cys residue is located in the C-terminal region of the analogue between a position corresp. to amino acid 251 and the C-terminus of ricin A chain. The analogues are pref. joined via a disulphide linkage to a molecule which specifically binds to a target cell, e.g. an antibody fragment.  
(Updated on 09-JAN-2003 to add missing OS field.)

(Updated on 25-MAR-2003 to correct PN field.)

SQ Sequence	267 AA;	Query Match Score 98.3%; Best Local Similarity 93.4%; Matches 185;	Score 934.5%; Pred. No. 2.3e-91;
		Conservative 0; Mismatches 0;	DB 14; Length 267;
		Indels 13; Gaps 1;	

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Qy      1 IFPKQYPIINFTTAGVQSYTNFTRAVGRILT-----NRVGLPINQRFLIV 47
Db      1 IFPKQYPIINFTTAGVQSYTNFTRAVGRILT-----NRVGLPINQRFLIV 60
Qy      48 ELSNFAELSVTLADVTNAYVVGTRAGNSAYFFHPDNOEDAITHLFTDVQNYTFAFG 107
Qy      61 ELSNFAELSVTLADVTNAYVVGTRAGNSAYFFHPDNOEDAITHLFTDVQNYTFAFG 120
Db      108 GNYDRLEQLAGNLRENLIGNGPLEAISALYYSTGGTQLPTLARSFTICIQMISEAR 167
Qy      121 GNYDRLEQLAGNLRENLIGNGPLEAISALYYSTGGTQLPTLARSFTICIQMISEAR 180
Db      168 FQYIEGEMRTRIYNRS 185
Qy      181 FQYIEGEMRTRIYNRS 198
Db      181 FQYIEGEMRTRIYNRS 198

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RESULT 2  
AAR63902 standard; Protein; 267 AA.  
XX AAR63902 ;  
AC AC  
DT 25-MAR-2003 (updated)  
DT 27-JUL-1995 (first entry)

DE Ricin A-chain (RTA).

XX Ricin A chain; RTA; ribosome-inactivating proteins; RIPS;  
KW Cytotoxic therapeutic agents; autoimmune disease; cancer;  
KW graft-versus-host disease.  
XX Ricinus communis.

OS WO9426910-A1.

XX 24-NOV-1994.

XX 12-MAY-1994; 94WO-US05348.  
XX 12-MAY-1993; 93US-0064691.

XX (XOMA ) XOMA CORP.

XX Better MD, Carroll SS, Studdicka GM, Carroll SF;  
XX DR; WPI: 1995-006804/01.

XX Polynucleotide(s) encoding type I ribosome-inactivating proteins

- which are suitable for use as components of cytotoxic therapeutic agents.

Example 3; Fig 1; 221pp; English.

XX AAR63902 is the ricin A chain gene product, it is analogous to the CC ribosome-inactivating proteins (RIPs) described in AAR63903-R63911. CC RIPS are the key components of cytotoxic therapeutic agents (CTAs), CC which include gene fusion products and immunoconjugates. CTAs may CC be used to selectively eliminate any cell type to which a RIP CC component is targeted, by the specific binding capacity of the CC second component of the agent. They can be used in the treatment CC of diseases where the elimination of particular cell type is CC desired, such as autoimmune disease, cancer and graft-versus-host CC disease;  
CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence	267 AA;	Query Match Score 98.3%; Best Local Similarity 93.4%; Matches 185;	Score 934.5%; Pred. No. 2.3e-91;
		Conservative 0; Mismatches 0;	DB 16; Length 267;
		Indels 13; Gaps 1;	

```

Qy      1 IFPKQYPIINFTTAGVQSYTNFTRAVGRILT-----NRVGLPINQRFLIV 47
Db      1 IFPKQYPIINFTTAGVQSYTNFTRAVGRILT-----NRVGLPINQRFLIV 60
Qy      48 ELSNFAELSVTLADVTNAYVVGTRAGNSAYFFHPDNOEDAITHLFTDVQNYTFAFG 107
Qy      61 ELSNFAELSVTLADVTNAYVVGTRAGNSAYFFHPDNOEDAITHLFTDVQNYTFAFG 120
Db      108 GNYDRLEQLAGNLRENLIGNGPLEAISALYYSTGGTQLPTLARSFTICIQMISEAR 167
Qy      121 GNYDRLEQLAGNLRENLIGNGPLEAISALYYSTGGTQLPTLARSFTICIQMISEAR 180
Db      168 FQYIEGEMRTRIYNRS 185
Qy      181 FQYIEGEMRTRIYNRS 198
Db      181 FQYIEGEMRTRIYNRS 198

```

RESULT 3

AAR25136 standard; Protein; 290 AA.  
ID AAW25136  
XX AAW25136;  
AC AAW25136;

XX DT 25-MAR-2003 (updated)  
DT 02-DEC-1997 (first entry)

DE Ricin A-chain ribosome inhibitory protein inactive precursor.  
XX Maize; PrRIP; ribosome inactivating protein; alpha; beta subunit;  
KW internal linker; Barley Translating Inhibitor; Trichosanthin;  
KW Ricin A-chain; Abrin-A A-chain; Saporin; SUT1; Luffin A; MAP;  
KW Ricinus communis; agglutinin; Momordin; PAP-S; Luffin-B; Dianthin 30;  
KW therapeutic toxin; tumour cell targeted; protein synthesis inhibitor;  
KW post-translational modification; cancer; neoplasia; HIV: AIDS;  
KW human immunodeficiency virus; acquired immune deficiency syndrome.  
XX OS Synthetic.  
XX PN US5646026-A.  
XX PD 08-JUN-1997.  
XX PF 07-JUN-1995; 95US-0485286.  
XX PR 09-DEC-1992; 92US-0987927.  
PR 11-JUN-1990; 90US-0535636.  
PR 26-JAN-1995; 95US-0378761.  
PR 07-JUN-1995; 95US-0485286.  
AX PA (DOWC ) DOWELANCO.

				/note= "Position of possible insertion of internal peptide linker sequence"
XX	Hey TD,	Morgan AER,	Walsh TA;	
PI				
XX	DR			
PT	1997-362934/33.			
XX	DNA encoding pro-ribosome inactivating proteins - inactive			
PT	PT precursors of ribosome inactivating proteins; can be expressed in eukaryotic cells without causing cell death			
XX	Claim 4; Column 91-94; 186PP; English.			
XX	AAW25136 represents a Ricin A-chain ribosome inhibitory protein (RIP) which was engineered to contain a selectively removable internal peptide linker sequence separating the alpha and beta units of the RIP. When separated the two units regain activity and are capable of inactivating eukaryotic ribosomes and hence preventing protein production. Many different RIPs may be produced with an internal linker including Maize RIP, Trichosanthin, Ricin A-chain, Abrin-A A-chain and Saporin. The RIPs can be used in the construction of therapeutic toxins targeted to specific cells such as tumour cells via the attachment of a targeting polypeptide, e.g. a monoclonal antibody. A further use is in HIV therapy (see US4869903). There is interest in expressing RIP recombinantly in host eukaryotic cells, because of the capacity to provide correct post-translational processing. However, RIPs effectively inhibit protein synthesis in eukaryotic cells resulting in cell death. Since the inactive RIP proteins are not cytotoxic to eukaryotic cells, they can be recombinantly expressed in such cells and then converted to active RIP proteins. However, (updated on 25-MAR-2003 to correct PP field.)			
XX	Sequence 290 AA;			
Qy	98.3%; Score 934.5; DB 18; Length 290; Best Local Similarity 93.4%; Pred. No. 2.5e-91; Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;			
Db	1 IPPKQYQPIINFATGATQSYNTNFTRAVGRIFT-----NRVGLPQNQRFLY 47 25 IPPKQYQPIINFATGATQSYNTNFTRAVGRIFTGADVRHEPVLPVRVGPPQNQRFLY 84			
Qy	48 ELSNHAELSVTIALDVINAYVGYRAGNSAYFFHPDNOEADAITHLFTDVONYRTFAFG 107 85 ELSNHAELSVTIALDVINAYVGYRAGNSAYFFHPDNOEADAITHLFTDVONYRTFAFG 144			
Db	Sequence 290 AA;			
Qy	98.3%; Score 934.5; DB 18; Length 290; Best Local Similarity 93.4%; Pred. No. 2.5e-91; Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;			
Db	1 IPPKQYQPIINFATGATQSYNTNFTRAVGRIFT-----NRVGLPQNQRFLY 47 25 IPPKQYQPIINFATGATQSYNTNFTRAVGRIFTGADVRHEPVLPVRVGPPQNQRFLY 84			
Qy	48 ELSNHAELSVTIALDVINAYVGYRAGNSAYFFHPDNOEADAITHLFTDVONYRTFAFG 107 85 ELSNHAELSVTIALDVINAYVGYRAGNSAYFFHPDNOEADAITHLFTDVONYRTFAFG 144			
Db	Sequence 290 AA;			
Qy	108 GNYDRLEQLAGNLRENLGNGPLEEAISALYYSTGGTOLPLTLARSFICIQMISEAAR 167 145 GNYDRLEQLAGNLRENLGNGPLEEAISALYYSTGGTOLPLTLARSFICIQMISEAAR 204			
Db	168 FOYIEGEMTRTRYNRRS 185 205 FOYIEGEMTRTRYNRRS 222			
RESULT 4	AAW21699			
XX	AAW21699 standard; Protein; 290 AA.			
XX	AC AAC70097;			RESULT 5
DT	25-MAR-2003 (updated)			AAP70097
DT	26-SEP-1997 (first entry)			ID AAP70097 standard; protein; 332 AA.
XX	Ricin A-chain RIP.			XX AC AAP70097;
XX	pro-Ribosome Inactivating Protein; PRORIP; peptide linker; cancer; inactivation; eukaryotic ribosome; alpha fragment; beta fragment; inhibitor; protein synthesis; N-glycosidase; glycosidic bond; liver; rat; ribosomal 28S RNA; cellular proliferation; HIV-infected T cell.			XX DT 09-APR-1991 (first entry)
OS	Ricinus communis.			XX DE Ricin A.
FH	Key Location/Qualifiers			
FT	Region 152..162			



DT	13-AUG-1990	(First entry)	QY	168 FQVIEGENMRTRYNRGS 185
XX	Ricin A encoded by insert from plasmid pRA123.		DB	216 FQVIEGENMRTRYNRGS 233
XX	Plasmid pRA123; ricin-A; ricin-B; cytotoxicity.			
XX	Ricinus communis.			
OS	Synthetic.			
XX		RESULT 8		
XX		AAR70827 standard; Protein; 554 AA.		
XX		ID AAR70827		
XX		XX		
XX		AC AAR70827;		
XX		XX		
XX		DT 25-MAR-2003 (updated)		
XX		JT 31-AUG-1995 (first entry)		
XX		XX		
DE	Anti-cataract immunotoxin.			
XX		XX		
XX	Immunotoxin; heavy chain; light chain; variable region; antibody; ricin-A; cytosolic; cataract; lens opacification; epithelial cell; PHB19; 4197X; monoclonal antibody; Mab.			
XX		XX		
PN	EP235476-A.			
XX		OS Synthetic.		
XX		XX		
PD	04-OCT-1989.	Location/Qualifiers		
XX		EH Key		
PF	19-JAN-1989;	PF Peptide		
XX	89EP-0201162.	FT 1..35	1..27	
XX		/label= leader sequence	/label= Sig_peptide	
FT	08-FEB-1984;	PR 084US-0578115.	/note= "phoA signal sequence"	
FT	08-FEB-1984;	PR 84US-0578121.	28..145	
FT	09-FEB-1984;	PR 84US-0578122.	/label= HEAVY	
PR	07-SEP-1984;	PR 84US-0648759.	/note= "Mab 4197X heavy chain"	
PR	20-SEP-1984;	PR 84US-0653515.	148..166	
XX		XX	/label= LINKER	
PA	(CETU ) CETUS CORPORATION.	PA /label= TAG	/label=	
XX		PA 169..274	note= "hexa-histidine tail"	
PI	Gelfand D, Lawyer FC, Horn G, Greenfield L, Nitecki D, Kaplan D;	FT /label= LIGHT		
PI	Piatak MJ;	FT note= "Mab 419X light chain"		
XX		FT Domain 276..544		
DR	WPI: 1989-286959/40.	FT Label= RICIN-A		
DR	N-PSDB; AAN91281.	FT 549..554		
XX		FT Peptide /label= TAG		
XX		FT note= "hexa-histidine tail"		
XX		FT /label=		
XX		FT Domain WO9503828-A1.		
XX		FT XX		
XX		PD 09-FEB-1995.		
XX		XX		
XX		PF 15-JUL-1994;	94WO-US07919.	
XX		XX		
XX		PR 02-AUG-1993;	93US-0101329.	
XX		XX		
XX		PD (HOU-) HOUSTON BIOTECHNOLOGY INC.		
XX		XX		
PI	Gould RM, Kelleher PJ, Wallace TL, Wood MS;	PI		
XX		XX		
XX		PR WPI: 1995-082036/11.		
XX		DR N-PSDB; AAQ85386.		
XX		XX		
PT	New single chain immuno:toxin - binds specifically to epithelial cells, for inhibiting development of sec. cataracts after extra:capsular cataract extraction.	PT		
XX		XX		
XX		XX Disclosure; Fig.4: 68pp; English.		
XX		XX		
CC	Plasmid RA123 (ATCC No. 39799) carries the entire coding sequence for ricin A, as well as codons for 12 AA's joining the A to the B chain.	CC	The immunotoxin given in AAR70827 comprises the heavy and light chain variable regions of anti-lens epithelium IgG3 Mab 4197X linked to ricin-A and a hexa-histidine tag. The DNA construct encoding the	
CC	Following modification for ease of manipulation the plasmid was used to construct expression vectors which express the conjugates in host cells.	CC	ricin toxin was expressed from PHB19 in E. coli.	
CC	(Updated on 31-OCT-2002 to add missing OS field.)	CC	(Updated on 25-MAR-2003 to correct PR field.)	
CC	(Updated on 25-MAR-2003 to correct PR field.)	CC	(Updated on 25-MAR-2003 to correct PR field.)	
CC	(Updated on 25-MAR-2003 to correct PR field.)	CC	(Updated on 25-MAR-2003 to correct PR field.)	
XX	Sequence 332 AA;	SQ	Sequence 554 AA;	
XX		Query Match 98.3%; Score 934.5; DB 10; Length 332;		
Best Local Similarity 93.4%; Pred. No. 3e-91; Mismatches 0; Indels 1;				
Matches 185; Conservative 0; Gaps 1;				
XX		XX Disclosure; Fig.4: 68pp; English.		
XX		XX		
QY	1 IFPKQPKIINPTTAGTVQSTNFTRAVRGSLT-----NRVGLPINKQRFLV 47	CC	The immunotoxin given in AAR70827 comprises the heavy and light chain variable regions of anti-lens epithelium IgG3 Mab 4197X linked to ricin-A and a hexa-histidine tag. The DNA construct encoding the	
Db	36 IFPKQPKIINPTTAGTVQSTNFTRAVRGSLTGAQVRIEIPVLPNRYGLPINKQRFLV 95	CC	ricin toxin was expressed from PHB19 in E. coli.	
QY	48 ELSNHAEISVTLADYTNAYVGYRAGNSAWFHDPNQEDEAITHLFTDVQNYRTFAFG 107	CC	(Updated on 25-MAR-2003 to correct PR field.)	
Db	96 ELSNHAEISVTLADYTNAYVGYRAGNSAWFHDPNQEDEAITHLFTDVQNYRTFAFG 155	CC	(Updated on 25-MAR-2003 to correct PR field.)	
QY	108 GNYDRLEQLAGNLRENTELGNGLPLEAISALUYYYSGGGTQPLTLARSFIICIQNSEAAR 167	SQ	Sequence 554 AA;	
Db	156 GNYDRLEQLAGNLRENTELGNGLPLEAISALUYYYSGGGTQPLTLARSFIICIQNSEAAR 215	Query Match 98.3%; Score 934.5; DB 16; Length 554;		
		Best Local Similarity 93.4%; Pred. No. 6e-91; Mismatches 0; Indels 13; Gaps 1;		

Qy	1 IFPKQPIINFTAGATVQSYTNTFIRAVGRIT-----NRVGLPINQRFILV 47	Db	96 ELSNHAELSVTLADVTNAVVGYRAGNSAYFFHDNQDAEATHLFTDVQNYTFAFG 155
Db	278 IFPKQPIINFTAGATVQSYTNTFIRAVGRITTGADYRHEIPVLNRVGFIDNQRFILV 337	Qy	108 GNYDRLEQLAGNLRENTIELNGNPLEEAISALYYSTGGTQPLTARSFLICIQMISEAAR 167
Qy	48 ELSNHAELSVTLADVTNAVVGYRAGNSAYFFHDNQDAEATHLFTDVQNYTFAFG 107	Db	156 GNYDRLEQLAGNLRENTIELNGNPLEEAISALYYSTGGTQPLTARSFLICIQMISEAAR 215
Db	338 ELSNHAELSVTLADVTNAVVGYRAGNSAYFFHDNQDAEATHLFTDVQNYTFAFG 397	Qy	168 FQYIEGEMTRIYNNRS 185
Qy	108 GNYDRLEQLAGNLRENTIELNGNPLEEAISALYYSTGGTQPLTARSFLICIQMISEAAR 167	Db	216 FQYIEGEMTRIYNNRS 233
Db	398 GNYDRLEQLAGNLRENTIELNGNPLEEAISALYYSTGGTQPLTARSFLICIQMISEAAR 457		
Qy	168 FQYIEGEMTRIYNNRS 185		
Db	458 FQYIEGEMTRIYNNRS 475		
			RESULT 10
			AAP50166 standard; Protein; 565 AA.
			AAP50166;
			AC XX
			XX DT 16-OCT-1991 (first entry)
			DE Sequence of preproricin encoded by PRCL617.
			XX DE
			XX Toxin; anti-tumour therapy.
			XX OS Ricinus.
			XX Key
			FR 1..24
			Peptide /label= signal
			FT 25..565
			Protein Region 292..303
			FT /label= links the C-terminus of the A chain and the N-terminus of the B chain
			FT Modified-site 34..36
			FT /label= N-linked glycosylation
			FT Modified-site 260..262
			FT /label= N-linked glycosylation
			FT Modified-site 398..400
			FT /label= N-linked glycosylation
			FT Modified-site 438..440
			FT /label= N-linked glycosylation
			XX PN EP145111-A.
			XX PD 19-JUN-1985.
			XX PF 13-JUL-1984; 84EP-0304801.
			XX PR 13-MAR-1984; 84GB-0006569.
			PR 15-JUL-1983; 83GB-001925.
			PR 15-JUL-1983; 83CH-001925.
			XX PA (UYWA-) UNIV WARWICK.
			AX Lord JM, Roberts LM, Lamb FI;
			XX WPI; 1985-148040/25.
			DR N-PSDB; AAN50202.
			XX PT New DNA sequences coding for ricin type plant toxin - or its mutants, and modified vectors and host microorganisms
			XX Disclosure; Fig 1; 51pp; English.
			PS PS
			XX Query Match 98.3%; Score 934.5; DB 10; Length 562;
			CC Best Local Similarity 93.4%; Pred. No. 6.1e-91; Indels 13; Gaps 1;
			CC Matches 185; Conservative 0; Mismatches 0;
Qy	1 IFPKQPIINFTAGATVQSYTNTFIRAVGRIT-----NRVGLPINQRFILV 47	CC	Ricin D (see Ricin. AAN90068) found on the EcoRI-HindIII fragment of DNA from Ricinus communis, Zanibarensis variety. Patent discloses many modifications of ricin in which the lectin binding function of the B chain is diminished or removed, and conjugation to toxins to eliminate cell binding.
		CC	PT Updated on 25-MAR-2003 to correct PA field.)
		CC	(Updated on 25-MAR-2003 to correct PI field.)
		XX	Sequence 562 AA;
		PS	XX
		CC	Query Match 98.3%; Score 934.5; DB 10; Length 562;
		CC	Best Local Similarity 93.4%; Pred. No. 6.1e-91;
		CC	Mismatches 0; Conservative 0; Indels 13; Gaps 1;
Qy	1 IFPKQPIINFTAGATVQSYTNTFIRAVGRIT-----NRVGLPINQRFILV 47	CC	Ricin D (see Ricin. AAN90068) found on the EcoRI-HindIII fragment of DNA from Ricinus communis, Zanibarensis variety. Patent discloses many modifications of ricin in which the lectin binding function of the B chain is diminished or removed, and conjugation to toxins to eliminate cell binding.
		CC	PT Updated on 25-MAR-2003 to correct PA field.)
		CC	(Updated on 25-MAR-2003 to correct PI field.)
		XX	Sequence 562 AA;
		PS	XX
		CC	Preproricin is the whole polypeptide encoded by AAN50202 and the DNA encoding this is claimed. Proricin is obtained from preproricin by removal of the B chain. The linker AA sequence which is present in the precursor polypeptide is enzymatically removed in the cell to separate the A and B chains, which are joined by a disulphide bridge during the formation of the ricin molecule itself.
		CC	This linker region as well as the presumptive amino terminal leader or signal sequence are not present in the sequences already published by Funatsu et al.
		CC	
Db	36 IFPKQPIINFTAGATVQSYTNTFIRAVGRITTGADYRHEIPVLNRVGFIDNQRFILV 95	CC	
Qy	48 ELSNHAELSVTLADVTNAVVGYRAGNSAYFFHDNQDAEATHLFTDVQNYTFAFG 107	CC	



PT	Protein	/label= HIV_protease_cleavage_site 304..565	25-MAR-2003 DT 21-MAY-1991 (updated) XX
PT		/label= Ricin B-chain /note= "Galactose/N-acetylgalactosamine-binding lectin"	Sequence of Ricinus communis (castor bean) Ricin toxin DE (RT or ricin) B precursor encoded by PRT38.
FT			DE XX
XX	WO200160393-A1.		KW Lectin; toxin protein; cytotoxic; cytostatic; castor bean; KW plant toxin.
PN			XX
XX	PD	23-AUG-2001.	Ricinus communis OS
XX	PF	15-FEB-2001; 2001WO-US05282.	XX
XX	PR	16-FEB-2000; 2000US-0182759.	FH Key Location/Qualifiers Region 1..35 /note= "leader"
XX	PA	(BECHT-) BECHTEL BWXT IDAHO LLC.	FT Region 36..302 /note= "A-chain"
XX	PI	KEENER WK, Ward TE;	FT Region 315..576 /note= "B-chain"
XX	PS	Example 1; Page 59-63; 66pp; English.	XX
XX	PT	Novel composition comprising toxin e.g., ricin based antiviral compound useful for treating viral infections such as human immunodeficiency virus infection.	XX
PT			PD 23-SEP-1987.
XX	PS		XX
XX	PT		PF 13-NOV-1986;
XX	PS		XX
XX	PT		PR 07-MAR-1986;
XX	PS		XX
CC	The sequence relates to the amino acid sequence of a modified proricin protein encoded by AA164145. The invention relates to a novel toxin (e.g. ricin) based antiviral agent which is toxic to virus-infected cells, but non-toxic to uninfected cells. The invention has anti-HIV and virucide activities. The agent is able to enter all HIV susceptible cells, and not just cells known to act as host cells for the virus. The antiviral agent remains inert in a cell unless the cell is infected with the HIV virus, where the viral protease activates it. Ricin's mechanism of action is through inactivation of cellular ribosomes and enhancement of binding of the antiviral agent to galactose residues on cell surfaces, and its cellular internalisation. The invention is useful for treating human immunodeficiency virus infection and other viral infections, especially retroviral infections. The antiviral agent is activated in viral particles or early-stage infected cells, killing the cells upon infection and effectively preventing the integration of the viral genome into the host genome thereby preventing the latency/rebound problem.	PA (CETUS CORP. PA (CHIRON CORP. XX	
XX	PS		PIatak M; XX
CC			DR WPI: 1987-265177/38. DR N-PSDE; AAN7056.
CC			XX
CC			New non-glycosylated ricin precursor and toxin etc. - are preprod. PT by recombinant DNA procedures with specific isolation steps for purer and soluble prods.
CC			XX
CC			Disclosure: Fig 14(1-2); 112PP; English.
CC			XX
CC			The full length sequences encoding ricin A (AAN70520), ricin D (AAN70525) putative ricin E (AAN70526) and RCA (AAN70524) in precursor form were obtained, using the messenger RNA to obtain a cDNA library, and then probing the library to retrieve the desired cDNA inserts. The, CC library was probed using the 35-mer given in AAN70514. Figure 4 (see AAN70520, AAN70521, AAN70522), shows the nucleotide sequences of three CC plasmids containing cDNA inserts obtained by Probing a cDNA library CC for sequences encoding ricin B using the probe in AAN70517. The cDNA CC inserts can be placed into expression vectors. Site-directed CC mutagenesis may be used to place an ARG start codon and a HindIII site at the beginning of the mature protein. (see AAN70518). The CC coding sequences of the inserts can be ligated into expression vectors. CC vectors containing the phoA promoter-operator and leader sequence CC (AAN70523) and suitable retroregulators. CC (Updated on 25-MAR-2003 to correct PA Field.)
XX	PS	Sequence 565 AA;	XX
QY		Query Match 98.3%; Score 934.5; DB 22; Length 565; Best Local Similarity 93.4%; Pred. No. 6..1e-91; Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;	Query Match 98.3%; Score 934.5; DB 8; Length 576; Best Local Similarity 93.4%; Pred. No. 6..3e-91; Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;
Db		1 IFPKQYPIINFATGATYQSYNTNFIRAVGRILT-----NRVGLPINQRFLV 47 25 IFPKQYPIINFATGATYQSYNTNFIRAVGRILTGADEVIFPVLPRVGFLPINQRFLV 84	1 IFPKQYPIINFATGATYQSYNTNFIRAVGRILT-----NRVGLPINQRFLV 47 36 IFPKQYPIINFATGATYQSYNTNFIRAVGRILTGADEVIFPVLPRVGFLPINQRFLV 95
QY		48 ELSNHAELSVTLADTVNAYVGYRAGNSAYFFHPDNEADAITHLFTDVONYRTFAFG 107 85 ELSNHAELSVTLADTVNAYVGYRAGNSAYFFHPDNEADAITHLFTDVONYRTFAFG 144	48 ELSNHAELSVTLADTVNAYVGYRAGNSAYFFHPDNEADAITHLFTDVONYRTFAFG 107 96 ELSNHAELSVTLADTVNAYVGYRAGNSAYFFHPDNEADAITHLFTDVONYRTFAFG 155
Db		108 GNYDRLEQAGNLRENTLNGPLEEALASALYYSTGGTQLPTLARSFIIQMISAAAR 167	108 GNYDRLEQAGNLRENTLNGPLEEALASALYYSTGGTQLPTLARSFIIQMISAAAR 167
QY		145 GNYDRLEQAGNLRENTLNGPLEEALASALYYSTGGTQLPTLARSFIIQMISAAAR 204	145 GNYDRLEQAGNLRENTLNGPLEEALASALYYSTGGTQLPTLARSFIIQMISAAAR 222
QY		168 FQV1GEGRTRIYNNRS 185	168 FQV1GEGRTRIYNNRS 222
Db		205 FQYEGEMRTRIYNNRS 185	205 FQYEGEMRTRIYNNRS 222
QY		RESULT 13 AAP70326 standard; Protein; 576 AA.	AAP70326 ID AAP70326 XX AC AC

Db	156 GNYDRLEQLAGNLRENILENGPLEERAISALYYSTGGTQIPLTARSFIICIQMISEAAR	215	CC delivery of agents (e.g. therapeutic genes, toxins, detectable CC labels) into cells. The use of a translocation mechanism ensures CC that the hybrid will be effective in relatively low doses, since a CC high proportion of the substance of interest will be taken into the CC targeted cells. The hybrid molecules can be manufactured as a CC single hybrid recombinant protein, permitting reproducibility, CC consistency, and the precise control of composition. CC (Updated on 25-MAR-2003 to correct PF field.)
XX	AAW25787 standard; Protein; 576 AA;	XX	
AC	AAW25787;	XX	
XX	25-MAR-2003 (updated)	DT	
DT	27-MAR-1998 (first entry)	XX	
DE	Castorbean ricin.	XX	
XX	Ricin; cytotoxin; hybrid protein; cell delivery; cell binding ligand; translocation domain; diphtheria toxin B'; interleukin-2; T-cell lymphoma; organ rejection; therapy.	XX	
XX	Ricinus communis.	OS	
XX	Key	Location/Qualifiers	
FT	Peptide	1..35	
FT	Protein	/label= Sig_peptide	
FT	Peptide	36..302	
FT	Peptide	/label= A-domain	
FT	Domain	303..314	
FT	Domain	315..576	
FT	Domain	/label= B-domain	
XX	PN	US5668255-A.	
XX	PD	16-SEP-1997.	
XX	PF	04-AUG-1993;	93US-0102387.
XX	PR	27-JUN-1991;	91US-0722484.
PR	07-JUN-1994;	94US-0618199.	
PR	25-APR-1995;	85US-0726808.	
PR	07-JUN-1995;	85US-0742554.	
PR	22-DEC-1999;	89US-0456695.	
PR	14-JUN-1990;	90US-0538216.	
PR	04-AUG-1993;	93US-0102387.	
XX	PA	(SERA-)	SERAGEN INC.
XX	PI	Murphy JR,	
XX	DR	WPI; 1997-470103/43.	
XX	N-PSDB:	AT91638.	
PT	New hybrid molecules for delivery of agents to cells - comprise a binding domain of a cell binding ligand and a portion of a translocation domain of a protein	XX	
PT	Example 4; Fig 11A-B; 30pp; English.	XX	
XX	This polypeptide comprises the castorbean cytotoxin, ricin, DNA (see AT91638) encoding the enzymatic A domain and a portion of the A-to-B linker peptide of ricin was used to construct a ricin-diphtheria toxin B'-interleukin-2 gene that was expressed in E. coli. The hybrid protein can be isolated and used to treat conditions involving over-production of cells bearing IL2 receptors, such as certain T-cell lymphomas and organ transplant rejection crises. The hybrid inactivates ribosomes in cells bearing IL2 receptors, resulting in cessation of protein synthesis and death of target cells. Claimed hybrid proteins comprise a translocation domain and a cell binding domain from e.g. a hormone, growth factor or polypeptide toxin. The hybrid molecules can be used for the	XX	

CC	delivery of agents (e.g. therapeutic genes, toxins, detectable labels) into cells. The use of a translocation mechanism ensures that the hybrid will be effective in relatively low doses, since a high proportion of the substance of interest will be taken into the targeted cells. The hybrid molecules can be manufactured as a single hybrid recombinant protein, permitting reproducibility, consistency, and the precise control of composition. (Updated on 25-MAR-2003 to correct PF field.)	XX	
XX	Sequence 576 AA;	Sequence	576 AA;
XX	Query Match 98.3%; Score 934.5; DB 18; Length 576;	Query	1 IFPKQYPINFTTAGTQSYTNTFIRAVGRPLT-----NRVCLPINORFILV 47
XX	Best Local Similarity 93.4%; Pred. No. 6.3e-91; Mismatches 0; Indels 13; Gaps 1;	Matches	185; Conservative 0;
XX	DB 36 IFPKQYPINFTTAGTQSYTNTFIRAVGRPLTGAIVRGRLTGADVRHEIPVLPNRYGLPINORFILV 95	Db	
XX	QY 48 ELSNHAEILSYTLADLVNTAVYGVAGNSAYFFHFDNQEDAATHLFTDVQNRTEAFG 107	Qy	
XX	DB 96 ELSNHAEILSYTLADLVNTAVYGVAGNSAYFFHFDNQEDAATHLFTDVQNRTEAFG 155	Db	
XX	QY 108 GNYDRLEQLAGNLRENTIELNGNPLEEAISALYYSTGGTOLPILTARSFTICIONMISEAAR 167	Qy	
XX	DB 156 GNYDRLEQLAGNLRENTIELNGNPLEEAISALYYSTGGTOLPILTARSFTICIONMISEAAR 215	Db	
XX	RESULT 15		
XX	AY55892 standard; protein; 576 AA.	ID	AY55892
XX	XX	XX	
XX	AC AAY55892;	AC	
XX	XX	XX	
XX	DT 15-FEB-2000 (first entry)	DT	
XX	XX	XX	
XX	DE Castor bean ricin toxin.	DE	
XX	XX	XX	
XX	Recombinant; hybrid; binding domain; ligand; animal cell; diphtheria; translocation domain; botulinum; neurotoxin; ricin; cholera; tetanus; shiga-like toxin; pertussis; translocation; cytoplasmic membrane; cytosol; therapy; genetic deficiency disease; enzyme; co-factor; poison; adipocyte; cancer; virus; infection; antibody.	XX	
XX	XX	XX	
XX	OS Ricinus communis.	OS	
XX	PN US565406-A.	PN	
XX	XX	XX	
XX	PD 12-OCT-1999.	PD	
XX	XX	XX	
XX	PF 07-JUN-1995;	PF	95US-0488246.
XX	XX	XX	
XX	PR 04-AUG-1993;	PR	93US-012387.
XX	XX	XX	
XX	PR 07-JUN-1984;	PR	84US-0618199.
XX	PR 27-JUN-1991;	PR	91US-0722484.
XX	PR 25-APR-1985;	PR	85US-0726808.
XX	PR 07-JUN-1985;	PR	85US-0742554.
XX	PR 22-DEC-1989;	PR	89US-0456695.
XX	PR 14-JUN-1990;	PR	90US-0538216.
XX	PA (SERA-)	PA	(SERA-) SERAGEN INC.
XX	Murphy JR,	XX	
XX	WPI; 1999-632431/54.	WPI	
XX	N-PSDB; AAZ30663.	N-PSDB	
XX	Recombinant DNA molecule encoding a three part hybrid protein used in the treatment of AIDS and genetic deficiency diseases -	PT	

## Example 4; Fig 11; 31pp; English.

XX  
 PS XX  
 CC The invention relates to a recombinant DNA molecule encoding a hybrid  
 CC protein comprising three parts: (a) the first part comprises a portion  
 CC of the bind-binding domain of a cell-binding polypeptide ligand allowing the  
 CC hybrid protein to bind to an animal cell; (b) the second part comprises  
 CC a portion of a translocation domain of a naturally occurring protein  
 CC selected from diphtheria toxin, botulinum neurotoxin, ricin, cholera  
 CC toxin, Lf toxin, C3 toxin, shiga-like toxin, pertussis toxin and tetanus  
 CC toxin, which translocate the third part of the across the cytoplasmic  
 CC membrane into the cytosol of the cell, and (c) the third part comprises  
 CC a polypeptide entity to be introduced into the cell, which is non-native  
 CC to the naturally occurring protein of (b). This sequence represents the  
 CC Castor bean ricin toxin sequence for use in generating the hybrid of the  
 CC invention. The hybrid molecule enables the direction of appropriate  
 CC therapy to affected cells, allowing them to function properly and  
 CC alleviate or cure the disease. The hybrid is especially used in treating  
 CC genetic deficiency diseases, by delivering to affected cells an enzyme  
 CC supplying the missing function, to supplementing cellular levels of a  
 CC particular enzyme or a scarce precursor or cofactor, to directing toxins  
 CC or other poisons to destroy particular cells (such as adipocytes, cancer  
 CC cell, or virus infected-cells), to counteracting viral infections such as  
 CC HIV, by introducing appropriate antibodies to viral proteins. It is also  
 CC involved in the process of getting non-therapeutic substances such as  
 CC detectable labels into cells.  
 XX

SQ Sequence 576 AA;

Query	Match	Score	Length
QY	1 IFPKQYPIINFATGATYSNTNPIRVRGLIT-----	98.3%	576
Db	36 IFPKQYPIINFATGATYSNTNPIRVRGLATGADVRHEIPVPLPNRGLPINQRFIV	93.4%	20
QY	48 ELSNHAEISVTLLADTVNAYVGTRAGNSAYFFPDPNQEDAEATHLFDVNQRYTAFG	93.4%	107
Db	96 ELSNHAEISVTLLADTVNAYVGTRAGNSAYFFPDPNQEDAEATHLFDVNQRYTAFG	6.3e-91	155
QY	108 GNYDRLEQLAGNRLENIELNGPLEEAISALYYSTGGTQLPTLARSFLICIONISEAR	0	167
Db	156 GNYDRLEQLAGNRLENIELNGPLEEAISALYYSTGGTQLPTLARSFLICIONISEAR	0	215
QY	168 FOYTEGEMTRIRYNNRS	1.85	233
Db	216 FOYTEGEMTRIRYNNRS	0	

Best Local Similarity Pred. No. Mismatches Indels Gaps  
 Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

----- NRVGLPINQRFIV 47  
 ----- NRVGLPINQRFIV 95

Search completed: February 10, 2004, 16:22:28  
 Job time : 31.5419 secs

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## OM protein - protein search, using sw model

Run on: February 10, 2004, 16:18:30 ; Search time 10.6968 Seconds  
 (Without alignments)  
 731.761 Million cell updates/sec

Title: US-10-083-336A-9  
 Perfect score: 951  
 Sequence: 1 IFPKQTEPIINFTAGATVQS.....ARFQYIEGEMTRIRYNRRS 185

Scoring table: BLOSUM62  
 Gapext 0.5 .

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/podata/1/iaa/5A-COMB.pep:\*
- 2: /cgn2\_6/podata/1/iaa/5B-COMB.pep:\*
- 3: /cgn2\_6/podata/1/iaa/6A-COMB.pep:\*
- 4: /cgn2\_6/podata/1/iaa/6B-COMB.pep:\*
- 5: /cgn2\_6/podata/1/iaa/pcutus-COMB.pep:\*
- 6: /cgn2\_6/podata/1/iaa/backfiles-COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	934.5	98.3	267	1	US-07-901-707-1
2	934.5	98.3	267	1	US-07-988-130-1
3	934.5	98.3	267	1	US-08-425-336-1
4	934.5	98.3	267	1	US-08-488-113B-1
5	934.5	98.3	267	1	US-08-477-184B-1
6	934.5	98.3	267	2	US-08-646-360-1
7	934.5	98.3	267	3	US-08-839-765-1
8	934.5	98.3	267	3	US-09-136-189-1
9	934.5	98.3	267	4	US-09-610-838-1
10	934.5	98.3	267	5	PCT-US92-09487-1
11	934.5	98.3	268	2	US-08-156-186-8
12	934.5	98.3	290	1	US-08-378-161A-27
13	934.5	98.3	290	1	US-08-485-286-27
14	934.5	98.3	290	6	5248606-4
15	924.5	97.2	267	1	US-08-356-786-10
16	924.5	97.2	267	1	US-08-218-103-16
17	924.5	97.2	267	2	US-08-338-193D-61
18	924.5	97.2	267	4	US-09-338-173-1
19	845	88.9	540	1	US-08-378-161A-77
20	845	88.9	540	1	US-08-445-286-77
21	337.5	35.5	247	1	US-08-488-113B-6
22	337.5	35.5	247	1	US-08-477-184B-6
23	337.5	35.5	247	2	US-08-646-360-6
24	337.5	35.5	247	3	US-08-839-765-6
25	337.5	35.5	247	3	US-09-136-189-6
26	337.5	35.5	247	4	US-09-610-838-6
27	337.5	35.5	267	1	US-08-378-161A-74

## 328717

## ALIGNMENTS

RESULT 1  
 US-07-901-707-1  
 Sequence 1, Application US/07901707

GENERAL INFORMATION:  
 Patent No. 5376546  
 APPLICANT: Bernhard, Susan L.  
 BETTER, Marc D.  
 APPLICANT: Carroll, Steve F.  
 APPLICANT: Lane, Julie A.  
 TITLE OF INVENTION: Materials Comprising and Methods of  
 Composition and Use for Ribosome-Inactivating Proteins  
 NUMBER OF SEQUENCES: 57

CURRENT APPLICATION DATA:  
 PRIORITY DATE: 1992-06-19

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

ADDRESSEE: Bicknell, Street

STREET: Two First National Plaza, 20 South Clark

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60603

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/901,707  
 FILING DATE: 1992-06-19  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/787,567  
 FILING DATE: 04-NOV-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: No. 5376546 and, Greta E.

REGISTRATION NUMBER: 35,302

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 346-5750  
 TELEFAX: (312) 984-5750  
 TELEX: 25-3856  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 267 amino acids  
 TYPE: AMINO ACID  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

US-07-901-707-1  
 Query Match 98.3%; Score 934.5; DB 1; Length 267;

Best Local Similarity 93.4%; Pred. No. 1.e-101; Mismatches 0; Indels 13; Gaps 1;

Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

Qy 1 IFPKQYPIINFTAGATYQSNTNFIAVRGLT-----NRVGLPINORFILY 47

Db 1 IFPKQYPIINFTAGATYQSNTNFIAVRGLTGAIVRHEIPVLPNVRGLPINQREFILY 60

Qy 48 ELSNHAEISVTIALDVTNAVVGYRAGNSAFFFHDNOEDAIAITHLFTDVNRYRAFG 107

Db 61 ELSNHAEISVTIALDVTNAVVGYRAGNSAFFFHDNOEDAIAITHLFTDVNRYRAFG 120

Qy 108 GNYDRLEQLAGNIRENTIELNGPLEEAISALYYSTGGTQLPTLARSFICQMSAAR 167

Db 121 GNYDRLEQLAGNIRENTIELNGPLEEAISALYYSTGGTQLPTLARSFICQMSAAR 180

Qy 168 FOYIEGMRTRIYNRS 185

Db 181 FOYIEGMRTRIYNRS 198

## RESULT 2

US-07-988-420-1

; Sequence 1, Application US/07988420

; Patent No. 5416202

; GENERAL INFORMATION:

; APPLICANT: Bernhard, Susan L.

; APPLICANT: Better, Marc D.

; APPLICANT: Carroll, Stephen F.

; APPLICANT: Lane, Julie A.

; APPLICANT: Lei, Shau-Ping

; TITLE OF INVENTION: Materials Comprising and Methods of Preparation and Use for Ribosome-Inactivating Proteins

; NUMBER OF SEQUENCES: 101

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borsun

; STREET: Two First National Plaza, 20 South Clark

; STREET: Street

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60603

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/988,430

FILING DATE: 1992-12-09

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/901,707

FILING DATE: 19-JUN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/787,567

FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: No. 5416202 and, Greta E.

REGISTRATION NUMBER: 35302

REFERENCE/DOCKET NUMBER: 31133

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 346-5750

TELEX: (312) 984-9740

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 267 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-07-988-420-1

## RESULT 3

US-08-425-336-1

; Sequence 1, Application US/08425336

; Patent No. 561083

; GENERAL INFORMATION:

; APPLICANT: Better, Marc D.

; APPLICANT: Carroll, Stephen F.

; APPLICANT: Studnitska, Gary M.

; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins

; NUMBER OF SEQUENCES: 140

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borsun

; STREET: 6300 Sears Tower, 233 South Wacker Drive

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/425,336

FILING DATE: 18-APR-1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/064,691

FILING DATE: 12-MAY-1993

APPLICATION NUMBER: US/07/901,707

FILING DATE: 19-JUN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/787,567

FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: Meyers, Thomas C.

REGISTRATION NUMBER: P-36,989

REFERENCE/DOCKET NUMBER: 31394

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/474-6300

TELEFAX: 312/474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 267 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-425-336-1

Query Match 98.3% Score 934.5% DB 1; Length 267;

Best Local Similarity 93.4%; Pred. No. 1.1e-101; Mismatches 0; Indels 13; Gaps 1;  
 Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-488-113B-1

Query Match 98.3%; Score 934.5%; DB 1; Length 267;  
 Best Local Similarity 93.4%; Prod. No. 1.1e-101;  
 Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;  
 Query Match 98.3%; Score 934.5%; DB 1; Length 267;  
 Best Local Similarity 93.4%; Prod. No. 1.1e-101;  
 Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

QY 1 IFPKQYPIINFTAGATVSYNTFRAVGRLT-----NRVGLPINORFLIV 47  
 DB 1 IFPKQYPIINFTAGATVSYNTFRAVGRLTGADYRHEIPVLPNRYGLPINORFLIV 60

QY 48 ELSNHAEISVTLLADTVNAYVGYRAGNSAYFFHPDNEQDAEATHLFTDVQNYRTFAFG 107  
 DB 61 ELSNHAEISVTLLADTVNAYVGYRAGNSAYFFHPDNEQDAEATHLFTDVQNYRTFAFG 120

QY 108 GNYDRLEQLAGNLRENIELGNGLPEEAISALYYSTGGTQLPLARSFTCIONQMISEAR 167  
 DB 121 GNYDRLEQLAGNLRENIELGNGLPEEAISALYYSTGGTQLPLARSFTCIONQMISEAR 180

QY 168 FOXYLEGEMTRTRYNRRS 185  
 DB 181 FOXYLEGEMTRTRYNRRS 198

RESULT 4  
 US-08-488-113B-1  
 Sequence 1, Application US/08488113B  
 Patent No. 5744380  
 GENERAL INFORMATION:  
 NUMBER OF SEQUENCES: 169  
 TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
 STREET: 500 West Madison Street, 34th floor  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: USA  
 ZIP: 60661

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/488.113B  
 FILING DATE: 07-JUN-1995  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/425,336  
 FILING DATE: 18-APR-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/064,691  
 FILING DATE: 12-MAY-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/988,430  
 FILING DATE: 09-DEC-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/901,707  
 FILING DATE: 19-JUN-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/187,567  
 FILING DATE: 04-NOV-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: McNicholas, Janet M.  
 REGISTRATION NUMBER: 32,918  
 REFERENCE/DOCKET NUMBER: 1.1022US07/200-70.P3.C2A  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 312/707-8889  
 TELEFAX: 312/707-9155  
 TELEX: 650 388-1248  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 267 amino acids

RESULT 5  
 US-08-477-488B-1  
 Sequence 1, Application US/08477484B  
 Patent No. 5756699  
 GENERAL INFORMATION:  
 APPLICANT: Better, Marc D.  
 ADDRESS: Carroll, Stephen F.  
 CITY: Studnitska, Gary M.  
 STATE: Immunotoxins Comprising Ribosome-Inactivating  
 COUNTRY: Proteins  
 NUMBER OF SEQUENCES: 169  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
 STREET: 500 West Madison Street, 34th floor  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: USA  
 ZIP: 60661  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/477,484B  
 FILING DATE: 07-JUN-1995  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/425,336  
 FILING DATE: 18-APR-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/064,691  
 FILING DATE: 12-MAY-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/988,430  
 FILING DATE: 09-DEC-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/901,707  
 FILING DATE: 19-JUN-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/988,430  
 FILING DATE: 04-NOV-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: McNicholas, Janet M.  
 REGISTRATION NUMBER: 32,918  
 REFERENCE/DOCKET NUMBER: 1.1022US07/200-70.P3.C2A  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 312/707-8889  
 TELEFAX: 312/707-9155  
 TELEX: 650 388-1248  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 267 amino acids

TELEPHONE: 312/707-8889  
 TELEFAX: 312/707-9155  
 TELEX: 650 388-1248  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 267 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

Query Match 98.3%; Score 934.5; DB 1; Length 267;  
 Best Local Similarity 93.4%; Pred. No. 1..1e-101;  
 Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

Qy 1 IFPKQYIPIINFTAGATVQSTNFTRAVGRLT-----NRVGLPINQRFILV 47  
 Db 1 IFPKQYIPIINFTAGATVQSTNFTRAVGRLT-----NRVGLPINQRFILV 60

Qy 48 ELSNHAELSVTLAIDVNTAYVGYDAGNSAYFFHPNQEDAATHLFTVQNYTFAFG 107  
 Db 61 ELSNHAELSVTLAIDVNTAYVGYDAGNSAYFFHPNQEDAATHLFTVQNYTFAFG 120

Qy 108 GNYDRQLQAGNLRENTELNGPLERAISSAYYYSTGGTQPLTARSFLCIONMISEAR 167  
 Db 121 GNYDRQLQAGNLRENTELNGPLERAISSAYYYSTGGTQPLTARSFLCIONMISEAR 180

Qy 168 FOYIEGMRTRIYRNRS 185  
 Db 181 FOYIEGMRTRIYRNRS 198

RESULT 6  
 US-08-646-360-1  
 Sequence 1, Application US/08646360  
 Patient No. 5337491  
 GENERAL INFORMATION:  
 APPLICANT: Carroll, Stephen F.  
 BETTER, Marc D.  
 TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
 NUMBER OF SEQUENCES: 173

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
 STREET: 500 West Madison Street, 34th Floor  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: USA  
 ZIP: 60661

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/646,360  
 FILING DATE: 13-MAY-1996  
 CLASSIFICATION: 530  
 PRIORITY APPLICATION DATA:  
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 FILING DATE: 12-MAY-1994  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/064,691  
 FILING DATE: 12-MAY-1993  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 07/988,430  
 FILING DATE: 09-DEC-1992  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 07/901,707  
 FILING DATE: 19-JUN-1992  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 07/787,567

RESULT 7  
 US-08-839-765-1  
 Sequence 1, Application US/08839765  
 Patient No. 6146631  
 GENERAL INFORMATION:  
 APPLICANT: Better, Marc D.  
 BETTER, Marc D.  
 APPLICANT: Carroll, Stephen F.  
 STUDNIKA, Gary M.  
 APPLICANT: Studnika, Gary M.  
 TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
 NUMBER OF SEQUENCES: 169  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
 STREET: 500 West Madison Street, 34th Floor  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: USA  
 ZIP: 60661

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/839,765  
 FILING DATE: 15-APR-1997  
 CLASSIFICATION: 530  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/425,336  
 FILING DATE: 18-APR-1995  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/064,691  
 FILING DATE: 12-MAY-1993  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/425,336  
 FILING DATE: 12-MAY-1993  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 07/988,430  
 FILING DATE: 19-JUN-1992  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 07/787,567

FILING DATE: 09-DEC-1992  
 PRIOR APPLICATION DATA:  
     APPLICATION NUMBER: US 07/901,707  
     FILING DATE: 19-JUN-1992  
 PRIOR APPLICATION DATA:  
     APPLICATION NUMBER: US 07/787,567  
     FILING DATE: 04-NOV-1991  
     ATTORNEY/AGENT INFORMATION:  
         NAME: McNicholas, Janet M.  
         REGISTRATION NUMBER: 32,918  
         REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3  
     TELECOMMUNICATION INFORMATION:  
         TELEPHONE: 312/707-8889  
         TELEFAX: 312/707-9155  
         TELEX: 650 388-1248  
     INFORMATION FOR SEQ ID NO: 1:  
         SEQUENCE CHARACTERISTICS:  
             LENGTH: 267 amino acids  
             TYPE: amino acid  
             TOPOLOGY: linear  
         MOLECULE TYPE: protein  
         S-08-839-765-1

Query Match	Score	Length	DB	Length	DB	Length	DB
Best Local Similarity	93.4%	Prod. No. 1.1e-10;	3	267	NRVGLPINQPFILV	47	1
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b	1 IFFKQPIINFTAGATQSYINPFRAVRGRLT-----NRVGLPINQPFILV						
Y	48 ELSNAEISVTLLAIDVNAYVVGAGRNSAYFFHPDQEDAAITHLIFTDVQNYTFAFG						
b	61 ELSNAEISVTLLAIDVNAYVVGAGRNSAYFFHPDQEDAAITHLIFTDVQNYTFAFG						
Y	108 GNYDRLQLAGNTRPENIELNGPLEAISALYYSTGCTQPLTARSFIIQTMISSEAR						
o	121 GNYDRLQLAGNTRPENIELNGPLEAISALYYSTGCTQPLTARSFIIQTMISSEAR						
Y	168 FQYIEGEMTRIRNRS 185						
c	181 FQYIEGEMTRIRNRS 198						

RESULT 8  
 S-09-136-389-1  
 Sequence 1, Application US/09-136389  
 Patent No. 6146550  
 GENERAL INFORMATION:  
     APPLICANT: Better, Marc D.  
     APPLICANT: Carroll, Stephen F.  
     APPLICANT: Studnka, Gary M.  
     TITLE OF INVENTION: Immunotoxin Comprising Ribosome-Inactivating  
     NUMBER OF SEQUENCES: 173  
     CORRESPONDENCE ADDRESS:  
         ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
         STREET: 500 West Madison Street, 34th Floor  
         CITY: Chicago  
         STATE: Illinois  
         COUNTRY: USA  
         ZIP: 60661  
     COMPUTER READABLE FORM:  
         MEDIUM TYPE: Floppy disk  
         COMPUTER: IBM PC compatible  
         OPERATING SYSTEM: PC DOS/MS-DOS  
         SOFTWARE: Patentin Release #1.0, Version #1.25  
     CURRENT APPLICATION DATA:  
         APPLICATION NUMBER: US/09/136,389  
         FILING DATE:  
         CLASSIFICATION:  
         PRIOR PUBLICATION DATA:  
             APPLICATION NUMBER: 08/646,360

OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/610,838  
 FILING DATE: 06-JUL-2000  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/09/136,389  
 FILING DATE: 18-AUG-1998  
 APPLICATION NUMBER: 08/546,360  
 FILING DATE: 13-MAY-1996  
 APPLICATION NUMBER: PCT/US94/05348  
 FILING DATE: 12-MAY-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/064,691  
 FILING DATE: 12-MAY-1993  
 APPLICATION DATA:  
 APPLICATION NUMBER: US 07/988,430  
 FILING DATE: 09-DEC-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/901,707  
 FILING DATE: 19-JUN-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/787,567  
 FILING DATE: 04-NOV-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: McNicholas, Janet M.  
 REGISTRATION NUMBER: 32,918  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 312/707-8889  
 TELEX: 650 388-1248  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 267 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-610-838-1

Query Match 98.3%; Score 934.5; DB 4; Length 267;

Best Local Similarity 93.4%; Pred. No. 1.1e-101; Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

Qy 1 IFPKQYPIINFATGATVQSYTINFIRAVGRIT-----NRVGLPINORFILV 47  
 Db 1 IFPKQYPIINFATGATVQSYTINFIRAVGRITGADVRHEIPVLNRGLPINORFILV 60  
 Qy 48 ELSNHAEISVTIALLDVINAYVGYRAGNSAYFFHPDNOEDAEITHLTDVQNYTEAFG 107  
 Db 61 ELSNHAEISVTIALLDVINAYVGYRAGNSAYFFHPDNOEDAEATHLFTDVQNYTEAFG 120  
 Qy 108 GNYDRLEQLAGNRLRENIELNGPLEEAISALYYSTGGTQLPLTLARSFIICIMISEAR 167  
 Db 121 GNYDRLEQLAGNRLRENIELNGPLEEAISALYYSTGGTQLPLTLARSFIICIMISEAR 180  
 Qy 168 FOYIEGEMTRTRYNEES 185  
 Db 181 FOYIEGEMTRTRYNEES 198

## RESULT 10

PCT-US92-09487-1  
 Sequence 1, Application PC/TUS9209487  
 GENERAL INFORMATION:  
 APPLICANT: Bernhard, Susan L.  
 BETTER, Marc D.  
 APPLICANT: Carroll, Stephen F.  
 APPLICANT: Lane, Julie A.  
 APPLICANT: Lei, Shau-Ping  
 TITLE OF INVENTION: Materials Comprising and Methods of Preparation and Use for Ribosome-Inactivating Proteins

## RESULT 11

US-08-356-386-8  
 Sequence 8, Application US/08356786  
 ; Sequence 8, Application US/08356786  
 ; Patent No. 5877305  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Huston, James S.  
 ; BETTER, Oppermann, Hermann  
 ; APPLICANT: Houston, L. L.  
 ; APPLICANT: Ring, David B.  
 ; TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer  
 ; TITLE OF INVENTION: Marker

NUMBER OF SEQUENCES: 16  
 CORRESPONDENCE ADDRESS:  
 ADDRESSE: Edmund R. Pitcher, Testa, Hurwitz, & Thibeault  
 STREET: Exchange Place, 53 State Street  
 CITY: Boston  
 STATE: Massachusetts  
 COUNTRY: USA  
 ZIP: 02109

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/356,786  
 FILING DATE: 06-FEB-1992  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/831,967  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Pitcher, Edmund R.  
 REGISTRATION NUMBER: 27,829  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 248-7000  
 TELEFAX: (617) 248-7100  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 268 amino acids  
 TYPE: amino acid  
 MOLECULE TYPE: protein  
 US-08-356-786-8

Query Match 98.3%; Score 934.5; DB 2; Length 268;  
 Best Local Similarity 93.4%; Pred. No. 1.1e-101;  
 Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

Qy 1 IFPKQYPIINFATGATVQSYNTNFIRAVGRIT-----NRVGLPINORFLIV 47  
 Db 25 IFPKQYPIINFATGATVQSYNTNFIRAVGRITGADVRHBIPLVNRVGLPINQFLV 84

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 Db 85 ELSNHAEISVTIADTVNAYVGYRAGNSAYFPHDNQEDAITHLFTDVQNYRTFAFG 144

Qy 108 GNYDRLEQLAGNLRENTLGNGPLEEAISALYYSTGTQLPTLARSFLICIQMISEAAR 167  
 Db 145 GNYDRLEQLAGNLRENTLGNGPLEEAISALYYSTGTQLPTLARSFLICIQMISEAAR 204

Qy 168 FOYIEGERMTRTRYNRS 185  
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RESULT 13  
 US-08-485-286-27  
 Sequence 27, Application US/08485286  
 ; Paten No. 5646026 5646119  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HEY, TIMOTHY D  
 ; APPLICANT: MORGAN, ALICE ER  
 ; APPLICANT: WALSH, TERENCE A  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: ANDREA T. BORUCKI  
 ; STREET: 9330 ZIONSVILLE ROAD  
 ; CITY: INDIANAPOLIS  
 ; STATE: IN  
 ; COUNTRY: US  
 ; ZIP: 46268

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/485,286  
FILING DATE: 4/3/5  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/378761  
FILING DATE: 26-JAN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: BORUCKI, ANDREA T.  
REGISTRATION NUMBER: 33651  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (317) 337-4846  
INFO FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 290 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-485-286-27

Query Match 98.3%; Score 934.5; DB 1; Length 290;  
Best Local Similarity 93.4%; Pred. No. 1.3e-101;  
Matches 185; Conservative 0; Mismatches 0;  
Indels 13; Gaps 1;

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Db 25 IFPKQYPIINFTTAGATVQSYTNFTRAVRGRLTGADVRHEIPVLPNRYGLPINQRFLIV 84  
Qy 48 ELSNHAEELSVTLADTVNAYVGYRAGNSAYFFHDNOEDAETHLFTDVQNYRTFAFG 107  
Db 85 ELSNHAEELSVTLADTVNAYVGYRAGNSAYFFHDNOEDAETHLFTDVQNYRTFAFG 144  
Qy 108 GNYDRLEQLAGNLRENIELGNGPLETEAISALYYSTGGTQLPTLARSFICIONTSEAR 167  
Db 145 GNYDRLEQLAGNLRENIELGNGPLETEAISALYYSTGGTQLPTLARSFICIONTSEAR 204  
Qy 168 FOYIEGMRTRIYRNRS 185  
Db 205 FOYIEGMRTRIYRNRS 222

RESULT 14  
;Patent No 5248606-4  
;APPLICANT: WALSH, TERENCE A.; HEY, TIMOTHY D.; MORGAN,  
;ALICE E.R.  
;TITLE OF INVENTION: DNA ENCODING INACTIVE PRECURSOR AND  
;ACTIVE FORMS OF MAIZE RIBOSOME INACTIVATIN  
;NUMBER OF SEQUENCES: 49  
;CURRENT APPLICATION DATA:  
;APPLICATION NUMBER: US/07/535,636  
;FILING DATE: 11-JUN-1990  
;SEQ ID NO: 4:  
;LENGTH: 290

5248606-4

Query Match 98.3%; Score 934.5; DB 6; Length 290;  
Best Local Similarity 93.4%; Pred. No. 1.3e-101;  
Matches 185; Conservative 0; Mismatches 0;  
Indels 13; Gaps 1;

Qy 1 IFPKQYPIINFTTAGATVQSYTNFTRAVRGRLT-----NRVGLPINQRFLIV 47  
Db 25 IFPKQYPIINFTTAGATVQSYTNFTRAVRGRLTGADVRHEIPVLPNRYGLPINQRFLIV 84  
Qy 48 ELSNHAEELSVTLADTVNAYVGYRAGNSAYFFHDNOEDAETHLFTDVQNYRTFAFG 107  
Db 64 ELSNHAEELSVTLADTVNAYVGYRAGNSAYFFHDNOEDAETHLFTDVQNYRTFAFG 123  
Qy 108 GNYDRLEQLAGNLRENIELGNGPLETEAISALYYSTGGTQLPTLARSFICIONTSEAR 167  
Db 124 GNYDRLEQLAGNLRENIELGNGPLETEAISALYYSTGGTQLPTLARSFICIONTSEAR 183  
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Db 184 FOYIEGMRTRIYRNRS 201

Sun Feb 15 07:30:06 2004

usb-10-083-336a-9.ra1

Page 9

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2004, 16:26:46 ; Search time 23.8621 Seconds  
(without alignments)  
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Title: US-10-083-336A-9

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Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

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18: /cgn2_6/ptodata/1/pubpa/US0_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
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3	939.5	98.8	189 12	Sequence 6, Appli
4	939.5	98.8	190 12	Sequence 11, Appli
5	934.5	98.3	198 12	Sequence 3, Appli
6	934.5	98.3	199 12	Sequence 5, Appli
7	934.5	98.3	200 12	Sequence 10, Appli
8	934.5	98.3	267 12	Sequence 1, Appli
9	934.5	98.3	576 12	Sequence 1, Appli
10	929.5	97.7	188 12	Sequence 8, Appli
11	924.5	97.2	198 12	Sequence 7, Appli
12	924.5	97.2	267 12	Sequence 1, Appli
13	924.5	97.2	267 12	Sequence 1, Appli
14	662.2	69.7	179 12	Sequence 2, Appli
15	337.5	35.5	247 12	Sequence 39, Appli

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the total score distribution, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	951.0	185	US-10-083-336A-9	Sequence 9, Appli
2	939.5	198.8	188 12	Sequence 4, Appli
3	939.5	98.8	189 12	Sequence 6, Appli
4	939.5	98.8	190 12	Sequence 11, Appli
5	934.5	98.3	198 12	Sequence 3, Appli
6	934.5	98.3	199 12	Sequence 5, Appli
7	934.5	98.3	200 12	Sequence 10, Appli
8	934.5	98.3	267 12	Sequence 1, Appli
9	934.5	98.3	576 12	Sequence 1, Appli
10	929.5	97.7	188 12	Sequence 8, Appli
11	924.5	97.2	198 12	Sequence 7, Appli
12	924.5	97.2	267 12	Sequence 1, Appli
13	924.5	97.2	267 12	Sequence 1, Appli
14	662.2	69.7	179 12	Sequence 2, Appli
15	337.5	35.5	247 12	Sequence 39, Appli

Sequence 6, Appli  
Sequence 39, Appli  
Sequence 4, Appli  
Sequence 34, Appli  
Sequence 34, Appli  
Sequence 3, Appli  
Sequence 3, Appli  
Sequence 7, Appli  
Sequence 4, Appli  
Sequence 2, Appli  
Sequence 8, Appli  
Sequence 5, Appli  
Sequence 107, Appli  
Sequence 106, Appli  
Sequence 110, Appli  
Sequence 111, Appli  
Sequence 247, Appli  
Sequence 2, Appli  
Sequence 99, Appli  
Sequence 100, Appli  
Sequence 101, Appli  
Sequence 102, Appli  
Sequence 103, Appli  
Sequence 104, Appli  
Sequence 105, Appli  
Sequence 11, Appli  
Sequence 109, Appli  
Sequence 259, Appli  
Sequence 253, Appli  
SEQUENCE  
ALIGNMENTS

RESULT 1  
US-10-083-336A-9  
; Sequence 9, Application US/10083336A  
; GENERAL INFORMATION:  
; Publication No. US20030181665A1  
; APPLICANT: Olson, Mark A.  
; APPLICANT: Millard, Charles B.  
; APPLICANT: Byrne, Michael P.  
; APPLICANT: Wannemacher, Robert W.  
; TIME OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof  
; FILE REFERENCE: P7452US0 (RIID 01-58)  
; CURRENT APPLICATION NUMBER: US/10/083,336A  
; CURRENT FILING DATE: 2002-05-21  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO: 9  
; LENGTH: 185  
; TYPE: PRT  
; ORGANISM: Ricinus communis  
US-10-083-336A-9

Query Match 100.0%; Score 951; Pred. No. 1.5e-101;  
Best Local Similarity 100.0%; Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query	Match	Length	DB	Score	Best Local Similarity	Matches	Conservative	Mismatches	Indels	Gaps	0;
1	IFPKQYPINFATGATVQSQS.....ARQYIEGEMRTRIYNRS	185	US-10-083-336A-9	QY	100.0%	1	1	0	0	0	;
2	LDVTNAYTVGYRAGNSAYFFHPDQNEADEATHLFTDVQRYTFAFGNYDRLEQLAGNL	185	US-10-083-336A-9	QY	100.0%	61	61	0	0	0	;
3	LDVTNAYTVGYRAGNSAYFFHPDQNEADEATHLFTDVQRYTFAFGNYDRLEQLAGNL	185	US-10-083-336A-9	Db	100.0%	61	61	0	0	0	;
4	LDVTNAYTVGYRAGNSAYFFHPDQNEADEATHLFTDVQRYTFAFGNYDRLEQLAGNL	185	US-10-083-336A-9	QY	100.0%	121	121	0	0	0	;
5	LDVTNAYTVGYRAGNSAYFFHPDQNEADEATHLFTDVQRYTFAFGNYDRLEQLAGNL	185	US-10-083-336A-9	Db	100.0%	121	121	0	0	0	;

181 YNRRS 185

Db 181 RIRYNRSS 185 .  
**RESULT 2**  
 US-10-083-336A-4  
 ; Sequence 4, Application US/10083336A  
 ; Publication No. US20030181665A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Olson, Mark A.  
 ; APPLICANT: Millard, Charles B.  
 ; APPLICANT: Byrne, Michael P.  
 ; APPLICANT: Wannemacher, Robert W.  
 ; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof  
 ; FILE REFERENCE: P67452US0 (RIID 01-58)  
 ; CURRENT APPLICATION NUMBER: US/10/083,336A  
 ; CURRENT FILING DATE: 2002-05-21  
 ; NUMBER OF SEQ ID NOS: 15  
 ; SOFTWARE: Patentin Ver. 2.1  
 ; SEQ ID NO: 4  
 ; LENGTH: 188  
 ; TYPE: PRT  
 ; ORGANISM: Ricinus communis  
 US-10-083-336A-4

Query Match 98.8%; Score 939.5; DB 12; Length 188;  
 Best Local Similarity 98.4%; Pred. No. 3.2e-100; Indels 3; Gaps 1;  
 Matches 185; Conservative 0; Mismatches 0; DB 12

Qy 1 IFPKQYPIINFTAGATVOSYTNTFIRAVRGRLT--NRYGLPINQRFILVELSNHAELSV 57  
 Db 1 IFPKQYPIINFTAGATVOSYTNTFIRAVRGRLT--NRYGLPINQRFILVELSNHAELSV 60  
 Qy 58 TLALDVTNAVVGYRAGNSAYFHPDQEAEATHLFTDVQRYTFAFGNYDRLEQLA 117  
 Db 61 TLALDVTNAVVGYRAGNSAYFHPDQEAEATHLFTDVQRYTFAFGNYDRLEQLA 120  
 Qy 118 GNRLRENLGNGPLEEALSALYYSTGTQLPTLARSFICTIONISEAARFQYEGEMRT 177  
 Db 121 GNRLRENLGNGPLEEALSALYYSTGTQLPTLARSFICTIONISEAARFQYEGEMRT 180  
 Qy 178 RIRYNRSS 185  
 Db 181 RIRYNRSS 188

Query Match 98.8%; Score 939.5; DB 12; Length 189;  
 Best Local Similarity 98.4%; Pred. No. 3.2e-100; Indels 3; Gaps 1;  
 Matches 185; Conservative 0; Mismatches 0; DB 12

Qy 1 IFPKQYPIINFTAGATVOSYTNTFIRAVRGRLT--NRYGLPINQRFILVELSNHAELSV 57  
 Db 1 IFPKQYPIINFTAGATVOSYTNTFIRAVRGRLT--NRYGLPINQRFILVELSNHAELSV 61  
 Qy 58 TLALDVTNAVVGYRAGNSAYFHPDQEAEATHLFTDVQRYTFAFGNYDRLEQLA 117  
 Db 62 TLALDVTNAVVGYRAGNSAYFHPDQEAEATHLFTDVQRYTFAFGNYDRLEQLA 121  
**RESULT 4**  
 US-10-083-336A-11  
 ; Sequence 11, Application US/10083336A  
 ; Publication No. US20030181665A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Olson, Mark A.  
 ; APPLICANT: Millard, Charles B.  
 ; APPLICANT: Byrne, Michael P.  
 ; APPLICANT: Wannemacher, Robert W.  
 ; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof  
 ; FILE REFERENCE: P67452US0 (RIID 01-58)  
 ; CURRENT APPLICATION NUMBER: US/10/083,336A  
 ; CURRENT FILING DATE: 2002-05-21  
 ; NUMBER OF SEQ ID NOS: 15  
 ; SOFTWARE: Patentin Ver. 2.1  
 ; SEQ ID NO: 11

Query Match 98.8%; Score 939.5; DB 12; Length 190;  
 Best Local Similarity 98.4%; Pred. No. 3.3e-100; Indels 3; Gaps 1;  
 Matches 185; Conservative 0; Mismatches 0; DB 12

Qy 1 IFPKQYPIINFTAGATVOSYTNTFIRAVRGRLT--NRYGLPINQRFILVELSNHAELSV 57  
 Db 2 IFPKQYPIINFTAGATVOSYTNTFIRAVRGRLT--NRYGLPINQRFILVELSNHAELSV 61  
 Qy 58 TLALDVTNAVVGYRAGNSAYFHPDQEAEATHLFTDVQRYTFAFGNYDRLEQLA 117  
 Db 62 TLALDVTNAVVGYRAGNSAYFHPDQEAEATHLFTDVQRYTFAFGNYDRLEQLA 121  
**RESULT 5**  
 US-10-083-336A-3  
 ; Sequence 3, Application US/10083336A  
 ; Publication No. US20030181665A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Olson, Mark A.  
 ; APPLICANT: Millard, Charles B.  
 ; APPLICANT: Byrne, Michael P.  
 ; APPLICANT: Wannemacher, Robert W.  
 ; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof  
 ; FILE REFERENCE: P67452US0 (RIID 01-58)  
 ; CURRENT APPLICATION NUMBER: US/10/083,336A  
 ; CURRENT FILING DATE: 2002-05-21  
 ; NUMBER OF SEQ ID NOS: 15  
 ; SOFTWARE: Patentin Ver. 2.1  
 ; SEQ ID NO: 11

Query Match 98.8%; Score 939.5; DB 12; Length 189;  
 Best Local Similarity 98.4%; Pred. No. 3.2e-100; Indels 3; Gaps 1;  
 Matches 185; Conservative 0; Mismatches 0; DB 12

Qy 1 IFPKQYPIINFTAGATVOSYTNTFIRAVRGRLT--NRYGLPINQRFILVELSNHAELSV 57  
 Db 1 IFPKQYPIINFTAGATVOSYTNTFIRAVRGRLT--NRYGLPINQRFILVELSNHAELSV 57

LENGTH: 198  
; TYPE: PRT ; ORGANISM: Ricinus communis  
US-10-083-336A-3

Query Match Score 934.5%; DB 12; Length 198;  
Best Local Similarity 93.4%; Pred. No. 1.3e-39;  
Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

Qy 1 IFPKQYPIINFTAGATVQSYNTNFIRAVRGRLT-----NRVGLPILNQRFILV 47  
Db 1 IFPKQYPIINFTAGATVQSYNTNFIRAVRGRLT-----NRVGLPILNQRFILV 60

Qy 48 ELSNHAEISVTALDVNTAYVGYRAGNSAYFFHPDNOEDAITHLFTDVQNRYTFAGF 1.07  
Db 61 ELSNHAEISVTALDVNTAYVGYRAGNSAYFFHPDNOEDAITHLFTDVQNRYTFAGF 120

Qy 108 GNYDRQLQAGNIRENIELNGNPLEEASALYYSTGGTQLETLARSFIICQMISEAR 1.67  
Db 121 GNYDRQLQAGNIRENIELNGNPLEEASALYYSTGGTQLETLARSFIICQMISEAR 1.80

Qy 168 FOYIEGEMTRTRYNRRS 185  
Db 181 FOYIEGEMTRTRYNRRS 198

RESULT 6  
US-10-083-336A-5

; Sequence 5, Application US/10083336A  
; Publication No. US20030181665A1  
; GENERAL INFORMATION:  
; APPLICANT: Olson, Mark A.  
; APPLICANT: Millard, Charles B  
; APPLICANT: Byrne, Michael P  
; APPLICANT: Wannemacher, Robert W  
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof  
; FILE REFERENCE: P67452US (RILD 01-58)  
; CURRENT APPLICATION NUMBER: US/10/083,336A  
; CURRENT FILING DATE: 2002-05-21  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 199  
; TYPE: PRT  
; ORGANISM: Ricinus communis  
US-10-083-336A-5

Query Match Score 934.5%; DB 12; Length 199;  
Best Local Similarity 93.4%; Pred. No. 1.3e-99;  
Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

Qy 1 IFPKQYPIINFTAGATVQSYNTNFIRAVRGRLT-----NRVGLIINQRFILV 47  
Db 2 IFPKQYPIINFTAGATVQSYNTNFIRAVRGRLT-----NRVGLIIPNQRFILV 61

Qy 48 ELSNHAEISVTALDVNTAYVGYRAGNSAYFFHPDNOEDAITHLFTDVQNRYTFAGF 1.07  
Db 62 ELSNHAEISVTALDVNTAYVGYRAGNSAYFFHPDNOEDAITHLFTDVQNRYTFAGF 121

Qy 108 GNYDRQLQAGNIRENIELNGNPLEEASALYYSTGGTQLETLARSFIICQMISEAR 1.67  
Db 122 GNYDRQLQAGNIRENIELNGNPLEEASALYYSTGGTQLETLARSFIICQMISEAR 1.81

Qy 168 FOYIEGEMTRTRYNRRS 185  
Db 182 FOYIEGEMTRTRYNRRS 199

RESULT 8  
US-10-127-890-1

; Sequence 1, Application US/10127890  
; Publication No. US20030166196A1  
; GENERAL INFORMATION:  
; SEQ ID NO 5  
; LENGTH: 199  
; TYPE: PRT  
; ORGANISM: Ricinus communis  
US-10-083-336A-5

Query Match Score 934.5%; DB 12; Length 199;  
Best Local Similarity 93.4%; Pred. No. 1.3e-99;  
Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

Qy 1 IFPKQYPIINFTAGATVQSYNTNFIRAVRGRLT-----NRVGLIINQRFILV 47  
Db 2 IFPKQYPIINFTAGATVQSYNTNFIRAVRGRLT-----NRVGLIIPNQRFILV 61

Qy 48 ELSNHAEISVTALDVNTAYVGYRAGNSAYFFHPDNOEDAITHLFTDVQNRYTFAGF 1.07  
Db 62 ELSNHAEISVTALDVNTAYVGYRAGNSAYFFHPDNOEDAITHLFTDVQNRYTFAGF 121

Qy 108 GNYDRQLQAGNIRENIELNGNPLEEASALYYSTGGTQLETLARSFIICQMISEAR 1.67  
Db 122 GNYDRQLQAGNIRENIELNGNPLEEASALYYSTGGTQLETLARSFIICQMISEAR 1.81

Qy 168 FOYIEGEMTRTRYNRRS 185  
Db 182 FOYIEGEMTRTRYNRRS 199

RESULT 17  
US-10-083-336A-10

; Sequence 10, Application US/10083336A  
; Publication No. US20030181665A1  
; GENERAL INFORMATION:

APPLICANT: Olson, Mark A.  
APPLICANT: Millard, Charles B  
APPLICANT: Byrne, Michael P  
APPLICANT: Wannemacher, Robert W  
TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof  
FILE REFERENCE: P67452US (RILD 01-58)  
CURRENT APPLICATION NUMBER: US/10/083,336A  
CURRENT FILING DATE: 2002-05-21  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 5  
LENGTH: 199  
TYPE: PRT  
ORGANISM: Ricinus communis  
US-10-083-336A-5

Query Match Score 934.5%; DB 12; Length 199;  
Best Local Similarity 93.4%; Pred. No. 1.3e-99;  
Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

Qy 1 IFPKQYPIINFTAGATVQSYNTNFIRAVRGRLT-----NRVGLIINQRFILV 47  
Db 2 IFPKQYPIINFTAGATVQSYNTNFIRAVRGRLT-----NRVGLIIPNQRFILV 61

Qy 48 ELSNHAEISVTALDVNTAYVGYRAGNSAYFFHPDNOEDAITHLFTDVQNRYTFAGF 1.07  
Db 62 ELSNHAEISVTALDVNTAYVGYRAGNSAYFFHPDNOEDAITHLFTDVQNRYTFAGF 121

Qy 108 GNYDRQLQAGNIRENIELNGNPLEEASALYYSTGGTQLETLARSFIICQMISEAR 1.67  
Db 122 GNYDRQLQAGNIRENIELNGNPLEEASALYYSTGGTQLETLARSFIICQMISEAR 1.81

Qy 168 FOYIEGEMTRTRYNRRS 185  
Db 182 FOYIEGEMTRTRYNRRS 199

APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992

APPLICATION NUMBER: US 07/787,567

FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: McNicholas, Janet M.

REGISTRATION NUMBER: 32,918

REFERENCE/DOCKET NUMBER: 200-70-P4

TELEPHONE: 312/707-8889

TELEFAX: 312/707-9155

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 267 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-10-127-850-1

Query Match Score 98.3%; Score 934.5; DB 12; Length 267;

Best Local Similarity 93.4%; Pred. No. 2e-99; Matches 0; Indels 13; Gaps 1;

Db 1 IFPKQYPIINFTTAGATYQSNTNFIRAVGRILT-----NRVGLPINQRFILV 47

Db 1 IFPKQYPIINFTTAGATYQSNTNFIRAVGRILT-----NRVGLPINQRFILV 60

Qy 48 ELSNHAEVLALDVTNAYVVGAGRNSAYFFHPDNOEDAATHLFTDVQNYRTFAFG 107

Db 61 ELSNHAEVLALDVTNAYVVGAGRNSAYFFHPDQDEAATHLFTDVQNYRTFAFG 120

Qy 108 GNYDRLEQLAGNRENIEELNGPLEAISALYYYSTGGTQLPLARSIFICIQMISBAAR 167

Db 121 GNYDRLEQLAGNRENIEELNGPLEAISALYYYSTGGTQLPLARSIFICIQMISBAAR 180

Qy 168 FOYIEGMRTRIYNRRS 185

Db 181 FOYIEGMRTRIYNRRS 198

RESULT 9  
US-10-083-336A-1

Sequence 1, Application US/10083336A

Publication No. US20030181665A1

GENERAL INFORMATION:

APPLICANT: Olson, Mark A

APPLICANT: Millard, Charles B

APPLICANT: Byrne, Michael P

APPLICANT: Wannemacher, Robert W

TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof

CURRENT APPLICATION NUMBER: US/10/083,336A

FILE REFERENCE: P67452US (RIID 01-58)

CURRENT FILING DATE: 2002-05-21

NUMBER OF SEQ ID NOS: 15

SOFTWARE: PatentIn Ver. 2.1

Qy 1 IFPKQYPIINFTTAGATYQSNTNFIRAVGRILT-----NRVGLPINQRFILV 47

Db 36 IFPKQYPIINFTTAGATYQSNTNFIRAVGRILT-----NRVGLPINQRFILV 95

Qy 48 ELSNHAEVLALDVTNAYVVGAGRNSAYFFHPDNOEDAATHLFTDVQNYRTFAFG 107

RESULT 11  
US-10-083-336A-7

Sequence 7, Application US/10083336A

Publication No. US20030181665A1

GENERAL INFORMATION:

APPLICANT: Olson, Mark A

APPLICANT: Millard, Charles B

APPLICANT: Byrne, Michael P

APPLICANT: Wannemacher, Robert W

TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof

FILE REFERENCE: P67452US (RIID 01-58)

CURRENT APPLICATION NUMBER: US/10/083,336A

FILE REFERENCE: P67452US (RIID 01-58)

CURRENT FILING DATE: 2002-05-21

NUMBER OF SEQ ID NOS: 15

SOFTWARE: PatentIn Ver. 2.1

Qy 1 IFPKQYPIINFTTAGATYQSNTNFIRAVGRILT-----NRVGLPINQRFILV 47

Db 36 IFPKQYPIINFTTAGATYQSNTNFIRAVGRILT-----NRVGLPINQRFILV 95

Qy 48 ELSNHAEVLALDVTNAYVVGAGRNSAYFFHPDNOEDAATHLFTDVQNYRTFAFG 107

US-10-083-336A-7

Query Match 97.2%; Score 924.5; DB 12; Length 198;  
 Best Local Similarity 93.4%; Pred. No. 1.9e-98;  
 Matches 183; Conservative 0; Mismatches 13; Gaps 1;  
 SEQ ID NO: 1

Qy 3 PKQYPLINTTAAATGATVQSYTNFIRAVRGLT-  
 Db 3 PKQYPLINTTAAATGATVQSYTNFIRAVRGLTGADRVHELPVLPRLPINKQFILVEL 62  
 Qy 50 SNAEALSVTLALDVNTAAYVVGAGRNSAYFFPDNQDAATHLFTDVNRGLT-  
 Db 63 SNAEALSVTLALDVNTAAYVVGAGRNSAYFFPDNQDAATHLFTDVNRGLTFAFGNN 122  
 Qy 110 YDRLEQLAGNLRENTIELNGPPEAISALYYSTGSGTQLPTLARSFICIQMISEARFQ 169  
 Db 123 YDRLEQLAGNLRENTIELNGPPEAISALYYSTGSGTQLPTLARSFICIQMISEARFQ 182  
 Qy 170 YIEGENRTTRIYNRRS 185  
 Db 183 YIEGENRTTRIYNRRS 198

RESULT 12 US-10-282-935-1  
 ; Sequence 1, Application US/10282935  
 ; GENERAL INFORMATION: Publication No. US20030143193A1  
 ; APPLICANT: VITETTA, ELLEN S.  
 ; APPLICANT: GHETTE, VICTOR F.  
 ; APPLICANT: SMALLSHAW, JOAN  
 ; APPLICANT: BALUNA, ROXANA G.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODIFYING TOXIC EFFECTS OF  
 ; FILE REFERENCE: US/10/282,935  
 ; CURRENT FILING DATE: 2002-10-29  
 ; PRIOR APPLICATION NUMBER: 09/538, 873  
 ; PRIOR FILING DATE: 1999-03-30  
 ; NUMBER OF SEQ ID NOS: 23  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO: 1  
 ; LENGTH: 267  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 ; OTHER INFORMATION: Peptide

US-10-282-935-1

Query Match 97.2%; Score 924.5; DB 12; Length 198;  
 Best Local Similarity 93.4%; Pred. No. 2.9e-98;  
 Matches 183; Conservative 0; Mismatches 13; Gaps 1;  
 SEQ ID NO: 1

Qy 3 PKQYPLINTTAAATGATVQSYTNFIRAVRGLT-  
 Db 3 PKQYPLINTTAAATGATVQSYTNFIRAVRGLTGADRVHELPVLPRLPINKQFILVEL 62  
 Qy 50 SNAEALSVTLALDVNTAAYVVGAGRNSAYFFPDNQDAATHLFTDVNRGLTFAFGNN 109  
 Db 63 SNAEALSVTLALDVNTAAYVVGAGRNSAYFFPDNQDAATHLFTDVNRGLTFAFGNN 122  
 Qy 110 YDRLEQLAGNLRENTIELNGPPEAISALYYSTGSGTQLPTLARSFICIQMISEARFQ 169  
 Db 123 YDRLEQLAGNLRENTIELNGPPEAISALYYSTGSGTQLPTLARSFICIQMISEARFQ 182  
 Qy 170 YIEGENRTTRIYNRRS 185  
 Db 183 YIEGENRTTRIYNRRS 198

RESULT 14 US-10-083-336A-2  
 ; Sequence 2, Application US/1008336A  
 ; GENERAL INFORMATION: Publication No. US20030181665A1  
 ; APPLICANT: Olson, Mark A.  
 ; APPLICANT: Millard, Charles B.  
 ; APPLICANT: Byrne, Michael P.  
 ; APPLICANT: Wannenacher, Robert W.  
 ; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof  
 ; FILE REFERENCE: P674520US0 (RIID 01-58)  
 ; CURRENT APPLICATION NUMBER: US/10/083,336A  
 ; CURRENT FILING DATE: 2002-05-21  
 ; NUMBER OF SEQ ID NOS: 15  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO: 2  
 ; LENGTH: 179  
 ; TYPE: PRT  
 ; ORGANISM: Ricinus communis

US-10-083-336A-2

Query Match 69.7%; Score 662.5; DB 12; Length 179;  
 Best Local Similarity 91.0%; Pred. No. 2.9e-68;  
 Matches 131; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

RESULT 13

Qy 1 IFPKQYPIINFTTAGATVOSYTNTFIRAYRGRLT-----NRVGLPINQRFLV 47  
 Db 36 IFPKQYPIINFTTAGATVOSYTNTFIRAYGRGLTGAHDVREIPVLPNRYGLPINQRFLV 95  
 Qy 48 ELSNHAEELSVTLADTYNAVYGRAGNSAYFFHDQNDEAITHLFTDVQNYTFAFG 107  
 Db 96 ELSNEAEELSVTLADTYNAVYGRAGNSAYFFHDQNDEAITHLFTDVQNYTFAFG 155  
 Qy 108 GNYDRLEQLAGNLRENTIELGNGPL 131  
 Db 156 GNYDRLEQLAGNLRENTIELGNGPL 179

RESULT 15

US-09-792-793A-39

; Sequence 39, Application US/09792793A

; Patent No. 0168370A1

; GENERAL INFORMATION:

; APPLICANT: McDonald, John R.

; APPLICANT: Coggins, Phillip

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND

; TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS

; FILE REFERENCE: 25020-601D

; CURRENT APPLICATION NUMBER: US/09/792,793A

; CURRENT FILING DATE: 2001-02-22

; NUMBER OF SEQ ID NOS: 93

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO: 39

; LENGTH: 247

; TYPE: PRT

; ORGANISM: Trichosanthus kirilowii

US-09-792-793A-39

Query Match Score 337.5; DB 10; Length 247;  
 Best Local Similarity 39.0%; Pred. No. 1.6e-30;  
 Matches 71; Conservative 42; Mismatches 50; Indels 19; Gaps 4;

Qy 9 INFETTAGATVOSYTNTFIRAYGRGLT-----RVGLPINQRFLVLSHAEISVT 58  
 Db 2 VSFRLSGATSSSYGVFSNLRCALPNERKLYDIPLRSSLGPSQYALHTNYADETIS 61  
 Qy 59 LAIDVINAYVVGGRAGNSAYFFHDQNDEAITHLFTDVQNYTFAFGNYDRLQLA 117  
 Db 62 VADIDVNVIIMMYRAGTSYF - NEASATEAKVFKDAMKTVLPSQNYERLQTA 118  
 Qy 118 GNLRNTELNGPLEEAIASALLYYSTGTOPLTLSFIIQMISEAARIQYIEGBMRT 177  
 Db 119 GKRENTPGLPGLDALSITLFIYAN ---SAASALMVLIQSTSEARVKFIEQIGK 173

Qy 178 RI 179

Db 174 RV 175

Search completed: February 10, 2004, 16:53:54  
 Job time : 23.8621 secs

Run on:	February 10, 2004, 16:17:35 ; Search time 10:0111 Seconds (without alignments) 1777.145 Million cell updates/sec	Score:	US-10-083-336A-9	Sequence:	951 1 IFPKQPLINTTAGATVQS..... .ARFQYIEGEMRTRIYNRRS 185	Scoring table:	BLOSUM62	Searched:	Gapext 0.5	Total number of hits satisfying chosen parameters:	283308
Minimum DB seq length:	0	Post-processing:	Maximum Match 0%	Database :	PIR_76:*	Result No.	Score	Query	Match Length	DB ID	Description
Maximum DB seq length:	2000000000	Maximum Match 100%	Listing first 45 summaries	1: pir1:*	1	934.5	98.3	576	1	RLCSD	ricin D precursor - castor bean
Post-processing:	Maximum Match 100%	Listing first 45 summaries	2: pir2:*	2	845.8	88.9	564	1	RLCSAG	N Contains: rRNA N-glycosidase (castor bean)	
Database :	PIR_76:*	3: pir3:*	3	327.5	35.5	289	1	RLTGG	C.Species: Ricinus communis (castor bean)		
Scoring table:	Gapext 0.5	4: pir4:*	4	327.5	34.4	247	2	JU0393	C.Date: 31-Dec-1993 #text change 16-Jul-1999		
Searched:	283308 seqs, 9618682 residues	Total number of hits satisfying chosen parameters:	283308	5	327.5	34.4	247	2	JCS032	CAccession: A24041; S20513; A24614; A03374; S10903	
Minimum DB seq length:	0	Post-processing:	Maximum Match 0%	6	327.5	34.4	289	2	JCS606	R.Halling, K.C.; Halling, A.C.; Murray, E.E.; Ladin, B.F.; Houston, L.L.; Weaver, R.F.	
Maximum DB seq length:	2000000000	Listing first 45 summaries	7	317.7	33.3	528	2	S32431	Nucleic Acids Res. 13, 8019-8033, 1985		
Post-processing:	Maximum Match 100%	Database :	8	317.7	33.3	562	2	S16022	A.Title: Genomic cloning and characterization of a ricin gene from Ricinus communis.		
Database :	PIR_76:*	9	316.5	33.3	527	2	S32430	A.Reference number: S20513; MUID:92163016; PMID:1299712			
Scoring table:	Gapext 0.5	10	310.0	32.6	251	2	C39761	A.Accession: A24041; MUID:86067214; PMID:2999712			
Searched:	283308 seqs, 9618682 residues	Total number of hits satisfying chosen parameters:	283308	11	297.1	31.2	278	2	S23519	A.Molecule type: DNA	
Minimum DB seq length:	0	Post-processing:	Maximum Match 0%	12	291.2	30.6	528	1	TZLSA	A.Residues: 1-576 <TRE>	
Maximum DB seq length:	2000000000	Listing first 45 summaries	13	290.1	30.5	250	2	JN0108	R.Jamb, F.I.; Roberts, L.M.; Lord, J.M.		
Post-processing:	Maximum Match 100%	Database :	14	276.4	29.0	277	2	S22494	A.Cross-references: EMBL:X52908; NID:921084; PID:CAA37095.1; PID:g21085		
Database :	PIR_76:*	15	272.5	28.7	254	2	PDD018	R.Tregear, J.W.; Roberts, I.M.			
Scoring table:	Gapext 0.5	16	270.5	28.4	286	1	RLPUGG	Eur. J. Biochem. 148, 265-270, 1985			
Searched:	283308 seqs, 9618682 residues	Total number of hits satisfying chosen parameters:	283308	17	268.5	28.2	295	2	S25560	A.Title: Nucleotide sequence of cloned cDNA coding for preproricin.	
Minimum DB seq length:	0	Post-processing:	Maximum Match 0%	18	268.5	28.2	570	2	S62627	A.Reference number: A24614; PMID:383723	
Maximum DB seq length:	2000000000	Listing first 45 summaries	19	266.5	28.0	245	2	JC4840	A.Accession: A24614		
Post-processing:	Maximum Match 100%	Database :	20	261.5	27.5	286	2	JC4235	A.Molecule type: protein		
Database :	PIR_76:*	21	279.0	28.7	316	2	JT0753	A.Residues: 36-97, Q-99-109, 'S', 111-269, 'D', 272-283, 'L', 285-290-302 <XOS>			
Scoring table:	Gapext 0.5	22	184.2	19.3	294	2	S28421	A.Note: this paper cites the others in the series providing experimental details for the			
Searched:	283308 seqs, 9618682 residues	Total number of hits satisfying chosen parameters:	283308	23	177.5	18.7	278	2	A39817	R.Yaraki, T.; Funatsu, G.	
Minimum DB seq length:	0	Post-processing:	Maximum Match 0%	24	168.5	17.7	313	2	S17757	FEBS Lett. 191, 121-124, 1985	
Maximum DB seq length:	2000000000	Listing first 45 summaries	25	167.6	17.6	261	2	JE0401	A.Title: Revised amino acid sequence of the B-chain of ricin D due to loss of tryptophan		
Post-processing:	Maximum Match 100%	Database :	26	150.0	15.8	289	2	T12573	A.Reference number: A24010		
Database :	PIR_76:*	27	138.5	14.6	272	2	JC4811	R.Toshihara, S.; Funatsu, G.; Funatsu, M.			
Scoring table:	Gapext 0.5	28	131.5	13.8	253	2	S28542	Agric. Biol. Chem. 42, 1267-1270, 1978			
Searched:	283308 seqs, 9618682 residues	Total number of hits satisfying chosen parameters:	283308	29	127.5	13.4	253	2	S28539	A.Title: Isolation and sequences of peptic peptides, and the complete sequence of Ile chitinase	
Minimum DB seq length:	0	Post-processing:	Maximum Match 0%							A.Reference number: A24372	
Maximum DB seq length:	2000000000	Listing first 45 summaries								A.Molecule type: protein	
Post-processing:	Maximum Match 100%	Database :								A.Residues: 12-75, 'D', 77-550, 'R', 552-576 <IAM>	
Database :	PIR_76:*									A.Cross-references: GB:X02388; NID:921077; PID:CAA262230.1; PID:g21078	
Scoring table:	Gapext 0.5									R.Toshihara, S.; Funatsu, G.; Funatsu, M.	
Searched:	283308 seqs, 9618682 residues	Total number of hits satisfying chosen parameters:	283308							A.Title: Nucleotide sequence of cloned cDNA coding for preproricin.	
Minimum DB seq length:	0	Post-processing:	Maximum Match 0%							A.Reference number: A24614	
Maximum DB seq length:	2000000000	Listing first 45 summaries								A.Molecule type: RNA	
Post-processing:	Maximum Match 100%	Database :								A.Residues: 1-576 <TRE>	
Database :	PIR_76:*									A.Cross-references: EMBL:X52908; NID:921084; PID:CAA37095.1; PID:g21085	
Scoring table:	Gapext 0.5									R.Jamb, F.I.; Roberts, L.M.; Lord, J.M.	
Searched:	283308 seqs, 9618682 residues	Total number of hits satisfying chosen parameters:	283308							A.Title: Isolation and sequences of peptic peptides, and the complete sequence of Ile chitinase	
Minimum DB seq length:	0	Post-processing:	Maximum Match 0%							A.Reference number: S20513; MUID:92163016; PMID:1299712	
Maximum DB seq length:	2000000000	Listing first 45 summaries								A.Molecule type: protein	
Post-processing:	Maximum Match 100%	Database :								A.Residues: 1-576 <TRE>	
Database :	PIR_76:*									A.Cross-references: EMBL:X52908; NID:921084; PID:CAA37095.1; PID:g21085	
Scoring table:	Gapext 0.5									R.Jamb, F.I.; Roberts, L.M.; Lord, J.M.	
Searched:	283308 seqs, 9618682 residues	Total number of hits satisfying chosen parameters:	283308							A.Title: Isolation and sequences of peptic peptides, and the complete sequence of Ile chitinase	
Minimum DB seq length:	0	Post-processing:	Maximum Match 0%							A.Reference number: S20513; MUID:92163016; PMID:1299712	
Maximum DB seq length:	2000000000	Listing first 45 summaries								A.Molecule type: protein	
Post-processing:	Maximum Match 100%	Database :								A.Residues: 1-576 <TRE>	
Database :	PIR_76:*									A.Cross-references: EMBL:X52908; NID:921084; PID:CAA37095.1; PID:g21085	
Scoring table:	Gapext 0.5									R.Jamb, F.I.; Roberts, L.M.; Lord, J.M.	
Searched:	283308 seqs, 9618682 residues	Total number of hits satisfying chosen parameters:	283308							A.Title: Isolation and sequences of peptic peptides, and the complete sequence of Ile chitinase	
Minimum DB seq length:	0	Post-processing:	Maximum Match 0%							A.Reference number: S20513; MUID:92163016; PMID:1299712	
Maximum DB seq length:	2000000000	Listing first 45 summaries								A.Molecule type: protein	
Post-processing:	Maximum Match 100%	Database :								A.Residues: 1-576 <TRE>	
Database :	PIR_76:*									A.Cross-references: EMBL:X52908; NID:921084; PID:CAA37095.1; PID:g21085	
Scoring table:	Gapext 0.5									R.Jamb, F.I.; Roberts, L.M.; Lord, J.M.	
Searched:	283308 seqs, 9618682 residues	Total number of hits satisfying chosen parameters:	283308							A.Title: Isolation and sequences of peptic peptides, and the complete sequence of Ile chitinase	
Minimum DB seq length:	0	Post-processing:	Maximum Match 0%							A.Reference number: S20513; MUID:92163016; PMID:1299712	
Maximum DB seq length:	2000000000	Listing first 45 summaries								A.Molecule type: protein	
Post-processing:	Maximum Match 100%	Database :								A.Residues: 1-576 <TRE>	
Database :	PIR_76:*									A.Cross-references: EMBL:X52908; NID:921084; PID:CAA37095.1; PID:g21085	
Scoring table:	Gapext 0.5									R.Jamb, F.I.; Roberts, L.M.; Lord, J.M.	
Searched:	283308 seqs, 9618682 residues	Total number of hits satisfying chosen parameters:	283308							A.Title: Isolation and sequences of peptic peptides, and the complete sequence of Ile chitinase	
Minimum DB seq length:	0	Post-processing:	Maximum Match 0%							A.Reference number: S20513; MUID:92163016; PMID:1299712	
Maximum DB seq length:	2000000000	Listing first 45 summaries								A.Molecule type: protein	
Post-processing:	Maximum Match 100%	Database :								A.Residues: 1-576 <TRE>	
Database :	PIR_76:*									A.Cross-references: EMBL:X52908; NID:921084; PID:CAA37095.1; PID:g21085	
Scoring table:	Gapext 0.5									R.Jamb, F.I.; Roberts, L.M.; Lord, J.M.	
Searched:	283308 seqs, 9618682 residues	Total number of hits satisfying chosen parameters:	283308							A.Title: Isolation and sequences of peptic peptides, and the complete sequence of Ile chitinase	
Minimum DB seq length:	0	Post-processing:	Maximum Match 0%							A.Reference number: S20513; MUID:92163016; PMID:1299712	
Maximum DB seq length:	2000000000	Listing first 45 summaries								A.Molecule type: protein	
Post-processing:	Maximum Match 100%	Database :								A.Residues: 1-576 <TRE>	
Database :	PIR_76:*									A.Cross-references: EMBL:X52908; NID:921084; PID:CAA37095.1; PID:g21085	
Scoring table:	Gapext 0.5									R.Jamb, F.I.; Roberts, L.M.; Lord, J.M.	
Searched:	283308 seqs, 9618682 residues	Total number of hits satisfying chosen parameters:	283308							A.Title: Isolation and sequences of peptic peptides, and the complete sequence of Ile chitinase	
Minimum DB seq length:	0	Post-processing:	Maximum Match 0%							A.Reference number: S20513; MUID:92163016; PMID:1299712	
Maximum DB seq length:	2000000000	Listing first 45 summaries								A.Molecule type: protein	
Post-processing:	Maximum Match 100%	Database :								A.Residues: 1-576 <TRE>	
Database :	PIR_76:*									A.Cross-references: EMBL:X52908; NID:921084; PID:CAA37095.1; PID:g21085	
Scoring table:	Gapext 0.5									R.Jamb, F.I.; Roberts, L.M.; Lord, J.M.	
Searched:	283308 seqs, 9618682 residues	Total number of hits satisfying chosen parameters:	283308							A.Title: Isolation and sequences of peptic peptides, and the complete sequence of Ile chitinase	
Minimum DB seq length:	0	Post-processing:	Maximum Match 0%							A.Reference number: S20513; MUID:92163016; PMID:1299712	
Maximum DB seq length:	2000000000	Listing first 45 summaries								A.Molecule type: protein	
Post-processing:	Maximum Match 100%	Database :								A.Residues: 1-576 <TRE>	
Database :	PIR_76:*									A.Cross-references: EMBL:X52908; NID:921084; PID:CAA37095.1; PID:g21085	
Scoring table:	Gapext 0.5									R.Jamb, F.I.; Roberts, L.M.; Lord, J.M.	
Searched:	283308 seqs, 9618682 residues	Total number of hits satisfying chosen parameters:	283308							A.Title: Isolation and sequences of peptic peptides, and the complete sequence of Ile chitinase	
Minimum DB seq length:	0	Post-processing:	Maximum Match 0%							A.Reference number: S20513; MUID:92163016; PMID:1299712	
Maximum DB seq length:	2000000000	Listing first 45 summaries								A.Molecule type: protein	
Post-processing:	Maximum Match 100%	Database :								A.Residues: 1-576 <TRE>	
Database :	PIR_76:*									A.Cross-references: EMBL:X52908; NID:921084; PID:CAA37095.1; PID:g21085	
Scoring table:	Gapext 0.5									R.Jamb, F.I.; Roberts, L.M.; Lord, J.M.	
Searched:	283308 seqs, 9618682 residues	Total number of hits satisfying chosen parameters:	283308							A.Title: Isolation and sequences of peptic peptides, and the complete sequence of Ile chitinase	
Minimum DB seq length:	0	Post-processing:	Maximum Match 0%							A.Reference number: S20513; MUID:92163016; PMID:1299712	
Maximum DB seq length:	2000000000	Listing first 45 summaries								A.Molecule type: protein	
Post-processing:	Maximum Match 100%	Database :								A.Residues: 1-576 <TRE>	
Database :	PIR_76:*									A.Cross-references: EMBL:X52908; NID:921084; PID:CAA37095.1; PID:g21085	
Scoring table:	Gapext 0.5									R.Jamb, F.I.; Roberts, L.M.; Lord, J.M.	
Searched:	283308 seqs, 9618682 residues	Total number of hits satisfying chosen parameters:	283308							A.Title: Isolation and sequences of peptic peptides, and the complete sequence of Ile chitinase	
Minimum DB seq length:	0	Post-processing:	Maximum Match 0%							A.Reference number: S20513; MUID:92163016; PMID:1299712	
Maximum DB seq length:	2000000000	Listing first 45 summaries								A.Molecule type: protein	
Post-processing:	Maximum Match 100%	Database :								A.Residues: 1-576 <TRE>	
Database :	PIR_76:*									A.Cross-references: EMBL:X52908; NID:921084; PID:CAA37095.1; PID:g21085	
Scoring table:	Gapext 0.5									R.Jamb, F.I.; Roberts, L.M.; Lord, J.M.	
Searched:	283308 seqs, 9618682 residues	Total number of hits satisfying chosen parameters:	283308							A.Title: Isolation and sequences of peptic peptides, and the complete sequence of Ile chitinase	
Minimum DB seq length:	0	Post-processing:	Maximum Match 0%							A.Reference number: S20513; MUID:92163016; PMID:1299712	
Maximum DB seq length:	2000000000	Listing first 45 summaries								A.Molecule type: protein	
Post-processing:	Maximum Match 100%	Database :								A.Residues: 1-576 <TRE>	
Database :	PIR_76:*									A.Cross-references: EMBL:X52908; NID:921084; PID:CAA37095.1; PID:g21085	
Scoring table:	Gapext 0.5									R.Jamb, F.I.; Roberts, L.M.; Lord, J.M.	
Searched:	283308 seqs, 9618682 residues	Total number of hits satisfying chosen parameters:	283308								

A;Residues: 315-335, 'N', 337-342, 'NH', 345-362, 364-383, 'PS', 386-399, 'T', 401, 'D', 403, 'E', 405, 'F', 407, 'W', 566, 'R', 567-570, 'L', 573-574, 'F' <FUN>  
 A;Note: this paper, one of a series, summarizes the experimental details for the determinants of Ricinus communis agglutinin.  
 R;Reedy, M.P.; Kim, Y.; Robertus, J.D.  
 Proteins 10, 270-278, 1991  
 A;Title: Site-directed mutagenesis of ricin A-chain and implications for the mechanism of action.  
 A;Reference number: A4827; PMID:91352006; PMID:18818833  
 A;Contents: annotation; X-ray crystallography; 2.5 angstroms  
 R;Katzin, B.J.; Collins, E.J.; Robertus, J.D.  
 Proteins 10, 251-259, 1991  
 A;Title: Structure of ricin A-chain at 2.5 angstroms.  
 A;Reference number: A48239; PMID:91352004; PMID:18818816  
 A;Contents: annotation; X-ray crystallography; 2.5 angstroms  
 C;Comment: The functional molecule is a disulfide-linked dimer of A and B chains, which inhibits protein synthesis; it inactivates the 60S ribosomal subunit of the cell of the A chain; B chains are also responsible for cell agglutination [lectin].  
 C;Comment: This protein is cytotoxic and very poisonous to animals.  
 C;Superfamily: ricin; RNA N-glycosidase homology  
 C;Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; RNA binding; seed protein; signal sequence; substrate predicted <SIG>  
 F:315-302/Product: ricin D chain A #status experimental <ACH>  
 F:315-293/Domain: RNA N-glycosidase homology <RNG>  
 F:315-576/Product: ricin D chain B #status experimental <BCH>  
 F:315-573/Domain: RNA N-glycosidase homology <RNG>  
 F:45-409, 449/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 F:115,158,143,24/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted  
 F:211/Active site: Arg #status predicted  
 F:294-418,34-353,377-394,465-478,504-521/Disulfide bonds: #status experimental  
 F:336,349,360/Binding site: N-acetylgalactosamine (Asp, Gln, Asn) #status experimental  
 F:548,569/Binding site: N-acetylgalactosamine (Asp, Asn) #status experimental

Query Match 98.3%; Score 93.4%; DB 1; Length 576;  
 Best Local Similarity 93.4%; Pred. No 2, 3e-78;  
 Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

Db 1 IPPKQYPIINFTAGATQSYTNFIRAVGRLT-----NRVGLPINQRFILY 47  
 Db 36 IPPKQYPIINFTAGATQSYTNFIRAVGRLT-----NRVGLPINQRFILY 95

Qy 48 ELSNHAELSVTLADVNAYVYGRAGNSAYFFHPDQEDAAITHLFTDVQRYTFAFG 107  
 Qy 96 ELSNHAELSVTLADVNAYVYGRAGNSAYFFHPDQEDAAITHLFTDVQRYTFAFG 155

Db 108 GNYDRLEQLAGNLRENTLEINGGLEEAISALYYSTGCTQLPTLARSPICIQMISEAAR 167  
 Db 156 GNYDRLEQLAGNLRENTLEINGGLEEAISALYYSTGCTQLPTLARSPICIQMISEAAR 215

Qy 168 FOYIEGMRTRIYNRRS 185  
 Db 216 FOYIEGMRTRIYNRRS 233

RESULT 3  
 PFLTZT

Qy 48 ELSNHAELSVTLADVNAYVYGRAGNSAYFFHPDQEDAAITHLFTDVQRYTFAFG 107  
 Qy 96 ELSNHAELSVTLADVNAYVYGRAGNSAYFFHPDQEDAAITHLFTDVQRYTFAFG 155

Db 108 GNYDRLEQLAGNLRENTLEINGGLEEAISALYYSTGCTQLPTLARSPICIQMISEAAR 167  
 Db 156 GNYDRLEQLAGNLRENTLEINGGLEEAISALYYSTGCTQLPTLARSPICIQMISEAAR 215

Qy 168 FOYIEGMRTRIYNRRS 185  
 Db 204 FOYIEGMRTRIYNRRS 221

R;Araki, T.; Yoshioka, Y.; Funatsu, G.  
 Biochim. Biophys. Acta 872, 277-285, 1986  
 A;Title: The complete amino acid sequence of the B-chain of the Ricinus communis agglutinin.  
 A;Reference number: A24210  
 A;Accession: A24210  
 A;Molecule type: protein  
 A;Residues: 303-321, 'F', 327-330, 'T', 332-361, 'D', 363-373, 'G', 375-403, 'T', 405-551, 'V', 553-C  
 C;Comment: This protein has strong agglutinating activity and weak cytotoxicity compared to ricin; RNA N-glycosidase homology  
 C;Superfamily: ricin; RNA N-glycosidase homology  
 C;Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; RNA binding; seed protein; signal sequence #status predicted <SIG>  
 F:25-290/Product: agglutinin chain A #status predicted <ACH>  
 F:35-281/Domain: RNA N-glycosidase homology <RNG>  
 F:303-564/Product: agglutinin chain B #status experimental <BCH>  
 F:319-361,362-402,405-443,450-485,489-528,531-564/Region: 40-residue repeats  
 F:34-259/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F:104,147,231,232/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted  
 F:200,203/Active site: Glu, Arg #status predicted  
 F:282-306,322-341,365-382,452-466,492-509/Disulfide bonds: #status predicted  
 F:324,337,348/Binding site: N-acetylglactosamine (Asp, Gln, Asn) #status predicted  
 F:397,437/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 F:535-557/Binding site: N-acetylglactosamine (Asp, Asn) #status predicted  
 Query Match 88.9%; Score 845; DB 1; Length 564;  
 Best Local Similarity 85.4%; Pred. No. 4e-70; B; Mismatches 7; Indels 14; Gaps 2;  
 Matches 169; Conservative 7;

Qy 1 IPPKQYPIINFTAGATQSYTNFIRAVGRLT-----NRVGLPINQRFILY 47  
 Qy 25 IPPKQYPIINFTAGATQSYTNFIRAVGRSLTGAIVRHEIPYLPNRVLGLPISQRFILY 84

Db 48 ELSNHAELSVTLADVNAYVYGRAGNSAYFFHPDQEDAAITHLFTDVQRYTFAFG 107  
 Db 85 ELSNHAELSVTLADVNAYVYGRAGNSAYFFHPDQEDAAITHLFTDVQNSTFAFG 144

Qy 108 GNYDRLEQLAGNLRENTLEINGGLEEAISALYYSTGCTQLPTLARSPICIQMISEAAR 167  
 Db 145 GNYDRLEQ-LGGLRENTLEINGGLEDAISALYYSTGCTQLPTLARSPICIQMISEAAR 203

RESULT 3  
 PFLTZT

RNA N-glycosidase (EC 3.2.2.22) alpha-trichosanthin precursor [validated] - Mongolian snake-gourd  
 N;Alternative names: alpha-TCS; type I ribosome-inactivating protein  
 C;Species: Trichosanthes kirilowii (Mongolian snake-gourd)  
 C;Date: 30-Sep-1988 #sequence\_revision 26-Jan-1996 #text\_change 23-Mar-2001  
 C;Accession: J070566; A36274; JC1099; A36273; JT0003  
 R;Shaw, P.C.; Yung, M.H.; Zhu, R.H.; Ho, W.K.K.; Ng, T.B.; Yeung, H.W.  
 Gene 97, 267-272, 1991  
 A;Title: Cloning of trichosanthin cDNA and its expression in Escherichia coli.  
 A;Reference number: JT0566; MUID:9153657; PMID:1999291  
 A;Accession: JT0566  
 A;Molecule type: mRNA  
 A;Residues: 1-289 <SHA>  
 A;Cross-references: GB:M34858; PID:9170536; PID:AAA34207.1; PID:9170537  
 A;Experimental source: tuber  
 R;Chow, T.P.; Feldman, R.A.; Lovett, M.; Piatak, M.  
 J.Biol. Chem. 265, 8670-8674, 1990  
 A;Title: Isolation and DNA sequence of a gene encoding alpha-trichosanthin, a type I ribonuclease from Trichosanthes kirilowii  
 A;Reference number: A36274; PMID:90256790  
 A;Molecule type: DNA  
 A;Residues: 1-233, 'T', 235-246, 'M', 248-289 <CHO>  
 A;Cross-references: GB:J05434; NID:9170534; PID:AAA34206.1; PID:9170535  
 R;Zheng, H.G.; Wang, B.; Shao, P.Z.; Yang, X.R.  
 A;Accession: A24261  
 A;Title: Cloning and DNA sequencing of the gene encoding Trichosanthin.  
 A;Reference number: JC1093; MUID:94271613; PMID:8003348  
 A;Accession: JC1093

A;Molecule type: DNA  
 A;Residues: 1'-2', 'V', 74-90, 'S', 92-233, 'T', 235-267, 'D', 269-289 <DHE>  
 A;Cross-references: GB:ST0176; NID:9547148; PID:547149  
 R;Collins, E.J.; Robertus, J.D.; LoPresti, M.; Stone, K.L.; Williams, K.R.; Wu, P.; Hwan J. Biol. Chem. 265, 8665-8669, 1990  
 A;Title: Primary amino acid sequences of alpha-trichosanthin and molecular models for abortive number: JU0393; MUID:92005521; PMID:1914000  
 A;Accession: JU0393  
 A;Molecule type: protein  
 A;Residues: 1-247 <TOY>  
 A;Note: a sequence which lacks Ala-247 is also shown in this publication  
 C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology  
 C;Keywords: abortifacient  
 F;4-243/Domain: rRNA N-glycosidase homology <RNG>

Query Match 34.4%; Score 327.5; DB 2; Length 247;  
 Best Local Similarity 39.0%; Pred. No. 8.6e-23;  
 Matches 42; Mismatches 50; Indels 19; Gaps 4;

Qy 9 INFTTAGATVQSYTNFIRAVRGRLTN-----RVGLPINQRFLVELSNHAEISVT 58  
 Db 2 VSPRLSGATSSSYGVFSNLKALPYERKLYDIPLRSTLPSQYRVALIHLTYADETIS 61

Qy 59 LALDTVNAYVGYGRAGNSAYFFPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLEQLA 117  
 Db 62 VAIDVTNVYVGYGRADTSYFF--NEASATEAAKYVKVTDKAKRVTLPYSQYRVLQIAA 118

Qy 118 GNLRNIELGNGLPEEALSAYYSTGGTQLPTLARSFLICIQMISEARFQYIEGENRT 177  
 Db 119 GKIRENIPGLPALSATIILFYNNAN---SAASALMVLIQSTSSEARYKFIEQIGK 173

RESULT 5  
 JC5032  
 karasurin-B - Trichosanthes kirilowii var. japonica  
 C;Species: Trichosanthes kirilowii var. japonica  
 C;Date: 27-Feb-1997 #sequence\_revision 27-Feb-1997 #text\_change 23-May-1997  
 C;Accession: JC5032  
 R;Kondo, T.; Mizukami, H.; Takeda, T.; Ogihara, Y.  
 Biol. Pharm. Bull. 19, 1485-1489, 1996  
 A;Title: Amino acid sequences and ribosome-inactivating activities of karasurin-B and karasurin-C  
 A;Reference number: JU0393; MUID:97108848; PMID:851169  
 A;Status: preliminary  
 A;Accession: JC5032  
 A;Molecule type: protein  
 A;Residues: 1-247 <KON>  
 C;Comment: This protein belongs to type I ribosomal-inactivating proteins which catalytic C;Superfamily: rRNA N-glycosidase homology <RNG>

Query Match 34.4%; Score 327.5; DB 2; Length 247;  
 Best Local Similarity 39.0%; Pred. No. 8.6e-23;  
 Matches 42; Mismatches 50; Indels 19; Gaps 4;

Qy 9 INFTTAGATVQSYTNFIRAVRGRLTN-----RVGLPINQRFLVELSNHAEISVT 58  
 Db 2 VSPRLSGATSSSYGVFSNLKALPYERKLYDIPLRSTLPSQYRVALIHLTYADETIS 61

Qy 59 LALDTVNAYVGYGRAGNSAYFFPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLEQLA 117  
 Db 62 VAIDVTNVYVGYGRADTSYFF--NEASATEAAKYVKVTDKAKRVTLPYSQYRVLQIAA 118

Qy 118 GNLRNIELGNGLPEEALSAYYSTGGTQLPTLARSFLICIQMISEARFQYIEGENRT 177  
 Db 119 GKIRENIPGLPALSATIILFYNNAN---SAASALMVLIQSTSSEARYKFIEQIGK 173

RESULT 4  
 JU0393  
 karasurin - Mongolian snake-gourd  
 C;Species: Trichosanthes kirilowii (Mongolian snake-gourd)

**RESULT 6**

A;Cross-references: GB:M98346  
 C;Comment: Abrin consists of an A chain, which inhibits protein synthesis by inactivating the A and B chains are linked by a single disulfide bond, which is essential for toxicity.  
 C;Superfamily: ricin; rRNA N-glycosidase homology  
 C;Keywords: disulfide bond; duplex; glycoprotein; glycosidase; hydrolase; lectin; p.  
 P:1-251/Product: abrin-c chain A #status predicted <ACH>  
 F:7-246/Domain: rRNA N-glycosidase homology <RNG>  
 C;Accession: JCS616; JCS533  
 C;Date: 23-Sep-1997 #sequence\_revision 23-Sep-1997 #text\_change 19-Jul-2002  
 C;Species: Trichosanthus kirilowii var. japonica  
 A;Title: Cloning and bacterial expression of a gene encoding ribosome-inactivating protein R;Mizukami, H.; Iida, K.; Kondo, T.; Oghara, Y.  
 Biol. Pharm. Bull. 20, 711-713, 1997  
 A;Reference number: JCS616; MUID:97356562; PMID:92129988  
 A;Accession: JCS606  
 A;Molecule type: DNA  
 A;Residues: 1-289 <MTZ>  
 A;Cross-references: DDBJ:AB000666; NID:G2329830; PIDN:BAA21786.1; PID:g2329831  
 R;Kondo, T.; Mizukami, H.; Takeda, T.; Ogihara, Y.  
 Biol. Pharm. Bull. 19, 1485-1489, 1996  
 A;Title: Amino acid sequences and ribosome-inactivating activities of karassurin-B and ka  
 A;Reference number: JCS5032; MUID:97108848; PMID:8951169  
 A;Accession: JCS5033  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 22-270 <KON>  
 C;Comment: This protein is a ribosome-inactivating protein and exhibit cytotoxic, aborti  
 C;Superfamily: type I ribosomal-inactivating Proteins which catalyti  
 C;Species: rRNA N-glycosidase; rRNA N-glycosidase homology  
 F:22-270/Product: karassurin C #status predicted <AAC>  
 F:24-270/Domain: karassurin A #status predicted <MAA>  
 F:27-266/Domain: rRNA N-glycosidase homology <RNG>  
 Query Match Score 34.4%; Score 327.5%; DB 2; Length 289;  
 Best Local Similarity 39.0%; Pred. No. 1.1e-22;  
 Matches 71; Conservative 42; Mismatches 50; Indels 19; Gaps 4;  
 Db 25 vsfrlsgatssygvflsnrlkalpkyerkldiprlrlstlpsqrvlyihlnyadetis 84

Qy 9 INFITAGATVQSYTNFIRAVGRQLTN-----RVGLPINORFILVELSNHAEISVT 58  
 Db 25 vsfrlsgatssygvflsnrlkalpkyerkldiprlrlstlpsqrvlyihlnyadetis 84

**RESULT 8**

Qy 59 1 LALDTVNAYVYGRAGNSAYFFPDNQEDA-FAITHLFTDVNRYTFAFGNNYDRLEQLA 117  
 Db 85 VADLTVNMYVGRAGDSYFF--NEASATAAKTYFKDARKVTLPSYNSYERLQIAA 141

Qy 118 GNLRENTIELNGPYLEEASALYYSTGGTQLPTLARSFLICIQMISPAARQYIEGEMRT 177  
 Db 142 GKIRENTPLGLFLDALSATIILFYNNAN---SAASALMVLIQSTSHEARYKFIEQQIK 196

Qy 178 RI 179  
 Db 197 RV 198

**RESULT 7**

S32431 abrin-D precursor - Indian licorice (fragment)  
 N;Contains: rRNA N-glycosidase (EC 3.2.2.22)  
 C;Species: Abrus precatorius (Indian licorice)  
 C;Date: 30-Sep-1993 #sequence\_revision 01-Aug-1997 #text\_change 01-Aug-1997  
 C;Accession: S32431; S34408  
 R;Hung, C.H.; Lee, M.-C.; Lee, T.C.; Lin, J.Y.  
 J. Mol. Biol. 229, 263-267, 1993  
 A;Title: Primary structure of three distinct isoabrins determined by cDNA sequencing.  
 A;Reference number: S32429; MUID:93132798; PMID:8421313  
 A;Accession: S32431  
 A;Molecule type: mrNA  
 A;Residues: 1-528 <HUN>  
 A;Cross-references: GB:M98346  
 R;Hung, C.; Lee, M.; Lee, T.; Lin, J.  
 submitted to the EMBL Data Library, March 1993  
 A;Reference number: S34408  
 A;Accession: S34408  
 A;Molecule type: mrNA  
 A;Residues: 1-169, 'C', 171-320, 'L', 322-528 <HU2>

Query Match Score 33.3%; Score 317; DB 2; Length 562;  
 Best Local Similarity 42.8%; Pred. No. 2.3e-21;  
 Matches 80; Conservative 23; Mismatches 66; Indels 18; Gaps 5;

Qy	5 QYPIINFTTAGTVQSYNTNFIRAVGRGLTNRV--GLPI-----NQRFILVELSNAH 53	Db	173 RVGVSRITN 181
Db	35 QDQVIKFTTGGATQSQYKOFTEALRRLTGGLIHDIPVLPPPTVEERNFTYTVLNSNE 94		RESULT 10
Qy	54 ELSVTLALDVNTAAYVYGRAGNSAYSFHDQNEDAAITHFLTDVQNYRTFAFGGNYDRL 113		C39761 abrin (clone 7.2) precursor - Indian licorice (fragment)
Db	95 RESIEVGIDVTNAYTAYVGRASSQSYL--RDAPASASTYLFPGTQ-RVSLRFDGSYGD 150		N; Contains: rRNA N-glycosidase (EC 3.2.2.22) C; Species: Abrin precursor (Indian licorice)
Qy	114 EQLAGNLRNIELNGPLEEAIASALYYSTGCGTQLPLARSFICIQMISEARFOYIEG 173		C; Date: 21-Feb-1992 #sequence_revision 31-Dec-1993 #text_change 20-Aug-1999
Db	151 ERWAHQTRTESSLGLQLALTHAIS--FLRSGASNDDEKARTLIVIQMASEARTRYISN 207		C; Accession: C39761; S1471 R; Evensen, G.; Mathiesen, A.; Sundan, A. J. Biol. Chem. 266, 6848-6852, 1991 A; Title: Direct molecular cloning and expression of two distinct abrin A-chains. A; Reference number: A39761; PMID:91201329; A; Accession: C39761 A; Molecule type: DNA A; Residues: 1-151 <EV2>
Qy	174 EMTRIR 180		R; Evensen, G.; Mathiesen, A.; Sundan, A. Submitted to the EMBL Data Library, October 1990 A; Description: Direct molecular cloning of two distinct abrin A-chains.
Db	208 RVGVSR 214		A; Accession: S14471 A; Molecule type: DNA A; Residues: 1-1251 <EV2>
RESULT 9	abrin-b precursor - Indian licorice (fragment)		A; Cross-references: EMBL:X54872; NID:gi16088; PID:CAA38654-1; PMID:gi16089
N; Contains: rRNA N-glycosidase (EC 3.2.2.22)			C; Superfamily: ricin; rRNA N-glycosidase homology
C; Species: Abrin precursor (Indian licorice)			C; Keywords: duplication; glycosidase; hydrolase; lectin; toxin
C; Accession: S32430; JC1399	#sequence_revision 01-Aug-1997 #text_change 20-Aug-1999		F1-1-251/Product: abrin (clone 7.2) chain A #status predicted <ACH>
C; Date: 30-Sep-1993 #sequence_revision 01-Aug-1997 #text_change 20-Aug-1999			F1-2-246/Domain: rRNA N-glycosidase homology < RNG >
C; Accession: S32430; JC1399			F74-113-195-196/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
C; Title: Primary structure of three distinct isoabkins determined by cDNA sequencing.			F164-167/Active site: Glu, Arg #status predicted
C; Accession: S32430			
A; Molecule type: mRNA			
A; Residues: 1-527 <HUN>			Query Match Score 32.6%; Pred. No. 3.6e-21;
A; Cross-references: GB:M98345; NID:gi166296; PID:AAA32625.1; PMID:9166297			Best Local Similarity 43.8%; Pred. No. 3.6e-21;
R; Kimura, M.; Sanizawa, T.; Funatsu, G.			Matches 81; Conservative 21; Mismatches 61; Indels 22; Gaps 6;
Biosci. Biotechnol. Biochem. 57, 165-169, 1993			
A; Title: The complete amino acid sequences of the B-chains of Abrin-a and Abrin-b, toxic			
A; Reference number: JC1398; PMID:7763422			
A; Molecule type: protein			Qy 9 INFETTAGTVQSYNTNFIRAVGRGLTNRVGL---PI-----NQRFILVELSNHAEL 55
A; Residues: 260-281, D', 283-290, 'N', 292-349, 'PQ', 352-377, 'N', 379-425, 'M', 427, 'D', 429-430			Db 5 KFSEBTGTSQSYKQFEALERL--RGGLTHDIPVLRLDPTVEERNRYTVELNSERE 62
A; Experimental source: seed			
C; Superfamily: ricin; rRNA N-glycosidase homology			Qy 56 SVTLLADVTNAYVYGRAGNSAYFFHDNQEDAEATHLFDVQNYRTFAFGGNYDRLEQ 115
C; Keywords: disulfide bond, duplication; glycoprotein; glycosidase; hydrolase; lectin; F			Db 63 SIEVGIDVTNAYVAVTGSQSYFL--RDAPASASTYLFGTQ-RYSLRDPGSYDLER 118
F7-245/Domain: rRNA N-glycosidase homology < RNG >			Qy 116 LAGNLRENIELNGPLEEAIASALYYSTGGTQLPLTARSFICIQMISEARFOYIEG 175
F260-527/Product: abrin-b chain B #status experimental < BCH >			Db 119 WAHQTRQISLGIQALTHAIS--FLRGASNDEEARTLIVIQMASEARFYRYSNRV 175
F1/Modified site: pyrrolidine carboxylic acid (Gln) #status predicted			
F74-113-194-195/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted			Qy 176 RTRIR 180
F110-163-166/Active site: Glu, Arg #status predicted			Db 176 GVJSR 180
F246-268-285-304-328-345-416-429, 455-472/Disulfide bonds: #status predicted			
F287-311/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted			RESULT 11
F499-520/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted			S23519
Query Match Score 33.3%; Pred. No. 2.3e-21;			beta-luffin - smooth loofah
Best Local Similarity 42.9%; Mismatches 23; Indels 19; Gaps 5;			C; Species: Luffa cylindrica (smooth loofah)
Matches 81; Conservative 23; Mismatches 66; Indels 19; Gaps 5;			C; Accession: S23519; S23113
Qy 5 QYPIINFTTAGTVQSYNTNFIRAVGRGLTNRV--GLPL-----NQRFILVELSNAH 53			R; Kataoka, J.; Babuka, N.; Miyano, M.; Masuta, C.; Koawai, A.
Db 1 QDQVIKFTTGGATQSQYKOFTEALRRLTGGLIHDIPVLPPPTVEERNFTYTVLNSNE 60			A; Title: Nucleotide sequence of cDNA encoding beta-luffin, another ribosome-inactivating
Qy 54 ELSVTLALDVNTAAYVYGRAGNSAYFFHDNQEDAEATHLFDVQNYRTFAFGGNYDRL 113			A; Reference number: S23519; PMID:921533400; PMID:1643290
Db 61 TESIAEGIDVTNAYVAVTGSQSYFL--RDAPASASTYLFGTQ-QSLLRPGNSYIDL 116			A; Molecule type: mRNA A; Residues: 1-278 <KAT>
Qy 114 EQLAGNLRNIELNGPLEEAIASALYYSTGGTQLPLTARSFICIQMISEARFOYIEG 173			A; Cross-references: EMBL:X62372; NID:gi19149; PID:CAA44230.1; PMID:919150
Db 117 ERLARQTRQISLGIQALTHAIS--QSGTDDQEARTLIVIQMASEARFYRYSY 172			C; Superfamily: rRNA N-glycosidase homology
Qy 174 EMTRIRYN 182	:		F26-264/Domain: rRNA N-glycosidase homology < RNG >
Query Match Score 31.2%; Pred. No. 6.6e-20;			Query Match Score 29%; DB 2;
Best Local Similarity 34.8%; Mismatches 45; Indels 18; Gaps 4;			Best Local Similarity 34.8%; Pred. No. 6.6e-20;
Matches 64; Conservative 64; Mismatches 57; Indels 18; Gaps 4;			Matches 64; Conservative 64; Mismatches 57; Indels 18; Gaps 4;

Qy 9 INFPTAGATVQSYTNTFIRAVGRGLTNR---VGLP1-----NORFILYELSNHAELSVT 58  
 A;Title: The complete primary structure of abrin-a B chain.  
 A;Reference number: S4133; MUID:92311656; PMID:150674  
 A;Accession: S24133  
 A;Molecule type: protein  
 A;Residues: 262-297, 'Y', 299-426, 'L', 428-466, 'P', 468-482, 'I', 484-528 <CHE>  
 R;Lin, S.H.; Chow, L.P.; Chen, Y.L.; Liaw, Y.C.; Chen, J.K.; Lin, J.Y.  
 Eur. J. Biochem. 240, 564-569, 1996  
 A;Title: Probing the domain structure of abrin-a by tryptic digestion.  
 A;Reference number: S74110; MUID:97008945; PMID:8856055  
 A;Accession: S74110  
 A;Molecule type: protein  
 A;Residues: 89-106; 154-172 <LINK>  
 A;Experimental source: seed  
 A;Accession: S74111  
 A;Molecule type: protein  
 A;Residues: 262-276, 'X', 278-280; 329-348; 369-388; 399-418 <LINK>  
 A;Experimental source: seed  
 C;Comment: Abrina is more toxic than ricin. The toxin consists of an A chain, which inhibiting receptors on the cell surface. The A and B chains are linked by a single disulfide bond.  
 C;Superfamily: ricin; rRNA N-glycosidase homology  
 C;Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; pyroglutamic acid  
 F;1:Species: Abrus precatorius (Indian licorice)  
 C;Date: 31-Dec-1993 #sequence revision 01-Aug-1997 #text\_change 16-Jul-1999  
 C;Accession: S24249; JT0202; A39761; JC1398; S14472; S24133; S74110; S74111  
 R;Hung, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.  
 J. Mol. Biol. 229, 263-257, 1993  
 A;Title: Primary structure of three distinct isoabrins determined by cDNA sequencing. Co  
 A;Reference number: S32429; MUID:93132798; PMID:B421313  
 A;Accession: S32429  
 A;Status: nucleic acid sequence not shown  
 A;Molecule type: mRNA  
 A;Residues: 'F', 2-528 <HIN>  
 A;Cross-references: GB:MB9344; NID:9166294; PID:9166295  
 A;Note: the coding region for the sequence is preceded by an ATG codon  
 A;Note: residues 1-8 were derived from the synthesized primer  
 R;Funatsu, G.; Taguchi, Y.; Kanenosono, M.; Yanaka, M.  
 Agric. Biol. Chem. 52, 1093-1097, 1988  
 A;Title: The complete amino acid sequence of the A-chain of abrin-a, a toxic protein from  
 A;Reference number: JT0202  
 A;Accession: JT0202  
 A;Molecule type: protein  
 A;Residues: 1-201; 203-251 <FUN>  
 A;Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have  
 R;Evensen, G.; Mathiesen, A.; Sundan, A.  
 J. Biol. Chem. 266, 6848-6852, 1991  
 A;Title: Direct molecular cloning and expression of two distinct abrin A-chains.  
 A;Reference number: A39761; MUID:91201329; PMID:2016300  
 A;Accession: A39761  
 A;Status: nucleic acid sequence not shown  
 A;Molecule type: DNA  
 A;Residues: 'B', 2-251 <EV>  
 A;Cross-references: GB:X54872  
 A;Note: residues 1-8 were derived from the synthesized primer  
 R;Kimura, M.; Sumizawa, T.; Funatsu, G.  
 Biosci. Biotechnol. Biochem. 57, 166-169, 1993  
 A;Title: The complete amino acid sequences of the B-chains of Abrin-a and Abrin-b, toxic  
 A;Reference number: JC1398; MUID:93169023; PMID:7763422  
 A;Contents: seeds  
 A;Accession: JC1398  
 A;Molecule type: protein  
 A;Residues: 261-347, 'T', 349-351, 'A', 353-357, 'L', 359-528 <KIM>  
 A;Experimental source: seed  
 R;Evensen, G.; Mathiesen, A.; Sundan, A.  
 Submitted to the EMBL Data Library, October 1990  
 A;Description: Direct molecular cloning of two distinct abrin A-chains.  
 A;Reference number: S14471  
 A;Accession: S14472  
 A;Status: Preliminary  
 A;Molecule type: DNA  
 A;Residues: 'ME', 2-251 <EV2>  
 A;Cross-references: EMBL:X54873; NID:916090; PID:CAA38655..1; PMID:916091  
 R;Chen, Y.L.; Chow, L.P.; Tsungita, A.; Lin, J.Y.

FIBS Lett. 309, 115-118, 1992  
 A;Title: The complete primary structure of abrin-a B chain.  
 A;Reference number: S4133; MUID:92311656; PMID:150674  
 A;Accession: S24133  
 A;Molecule type: protein  
 A;Residues: 262-297, 'Y', 299-426, 'L', 428-466, 'P', 468-482, 'I', 484-528 <CHE>  
 R;Lin, S.H.; Chow, L.P.; Chen, Y.L.; Liaw, Y.C.; Chen, J.K.; Lin, J.Y.  
 Eur. J. Biochem. 240, 564-569, 1996  
 A;Title: Probing the domain structure of abrin-a by tryptic digestion.  
 A;Reference number: S74110; MUID:97008945; PMID:8856055  
 A;Accession: S74110  
 A;Molecule type: protein  
 A;Residues: 89-106; 154-172 <LINK>  
 A;Experimental source: seed  
 A;Accession: S74111  
 A;Molecule type: protein  
 A;Residues: 262-276, 'X', 278-280; 329-348; 369-388; 399-418 <LINK>  
 A;Experimental source: seed  
 C;Comment: Abrina is more toxic than ricin. The toxin consists of an A chain, which inhibiting receptors on the cell surface. The A and B chains are linked by a single disulfide bond.  
 C;Superfamily: ricin; rRNA N-glycosidase homology  
 C;Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; pyroglutamic acid  
 F;1:Species: Abrus precatorius (Indian licorice)  
 C;Date: 31-Dec-1993 #sequence revision 01-Aug-1997 #text\_change 16-Jul-1999  
 C;Accession: S24249; JT0202; A39761; JC1398; S14472; S24133; S74110; S74111  
 R;Hung, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.  
 J. Mol. Biol. 229, 263-257, 1993  
 A;Title: Primary structure of three distinct isoabrins determined by cDNA sequencing. Co  
 A;Reference number: S32429; MUID:93132798; PMID:B421313  
 A;Accession: S32429  
 A;Status: nucleic acid sequence not shown  
 A;Molecule type: mRNA  
 A;Residues: 'F', 2-528 <HIN>  
 A;Cross-references: GB:MB9344; NID:9166294; PID:9166295  
 A;Note: the coding region for the sequence is preceded by an ATG codon  
 A;Note: residues 1-8 were derived from the synthesized primer  
 R;Funatsu, G.; Taguchi, Y.; Kanenosono, M.; Yanaka, M.  
 Agric. Biol. Chem. 52, 1093-1097, 1988  
 A;Title: The complete amino acid sequence of the A-chain of abrin-a, a toxic protein from  
 A;Reference number: JT0202  
 A;Accession: JT0202  
 A;Molecule type: protein  
 A;Residues: 1-201; 203-251 <FUN>  
 A;Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have  
 R;Evensen, G.; Mathiesen, A.; Sundan, A.  
 J. Biol. Chem. 266, 6848-6852, 1991  
 A;Title: Direct molecular cloning and expression of two distinct abrin A-chains.  
 A;Reference number: A39761; MUID:91201329; PMID:2016300  
 A;Accession: A39761  
 A;Status: nucleic acid sequence not shown  
 A;Molecule type: DNA  
 A;Residues: 'B', 2-251 <EV>  
 A;Cross-references: GB:X54872  
 A;Note: residues 1-8 were derived from the synthesized primer  
 R;Kimura, M.; Sumizawa, T.; Funatsu, G.  
 Biosci. Biotechnol. Biochem. 57, 166-169, 1993  
 A;Title: The complete amino acid sequences of the B-chains of Abrin-a and Abrin-b, toxic  
 A;Reference number: JC1398; MUID:93169023; PMID:7763422  
 A;Contents: seeds  
 A;Accession: JC1398  
 A;Molecule type: protein  
 A;Residues: 261-347, 'T', 349-351, 'A', 353-357, 'L', 359-528 <KIM>  
 A;Experimental source: seed  
 R;Evensen, G.; Mathiesen, A.; Sundan, A.  
 Submitted to the EMBL Data Library, October 1990  
 A;Description: Direct molecular cloning of two distinct abrin A-chains.  
 A;Reference number: S14471  
 A;Accession: S14472  
 A;Status: Preliminary  
 A;Molecule type: DNA  
 A;Residues: 'ME', 2-251 <EV2>  
 A;Cross-references: EMBL:X54873; NID:916090; PID:CAA38655..1; PMID:916091  
 R;Chen, Y.L.; Chow, L.P.; Tsungita, A.; Lin, J.Y.

Query Match 30.5%; Score 290; DB 2; Length 250;  
 RESULT 13  
 JN0108 luffin-b - smooth loofah  
 C;Species: Luffa cylindrica (smooth loofah)  
 C;Date: 04-Sep-1998 #sequence\_revision 04-Sep-1998 #text\_change 07-May-1999  
 C;Accession: JN0108  
 R;Islam, M.R.; Hirayama, H.; Funatsu, G.  
 Agric. Biol. Chem. 55, 229-238, 1991  
 A;Title: Complete amino acid sequence of luffin-b, a ribosome-inactivating protein from  
 A;Reference number: JN0108; MUID:91248488; PMID:1368666  
 A;Accession: JN0108  
 A;Molecule type: protein  
 A;Residues: 1-250 <ISI>  
 C;Superrfamily: rRNA N-glycosidase homology  
 C;Domain: rRNA N-glycosidase homology <RNG>  
 Query Match 30.5%; Score 290; DB 2; Length 250;

Best Local Similarity 33.2%; Pred. No. 2.5e-19; Matches 61; Conservative 48; Mismatches 57; Indels 18; Gaps 4;	Qy 9 INFETAGATVQSYTINFIRAVRGRLLTNVGLPIN-----QRFLIVELSNHAELSV 57 Db 22 VRFSEISGSSSTSYKFEIGURKALPSN-STVVYNTULLSSASGASRYTTMLSNYDKRAI 80
Qy 9 INFETAGATVQSYTINFIRAVRGRLLTR--VGLPI-----INQRFILVELSNHAELSV 58 Db 3 VSFISLGADSKSYSKSKEITLRLKPKEXVSNIPILLPSASGSARYTILMOLSNYDAKAI 62	Qy 58 TLALDVTNAYTVGTRAGNSAYFFHPDNQDAEAATHLFIDVQNYTFAGFGNYDRLEQIA 117 Db 81 TVADVDTNVTYMGVLVNSTSYFF--NESDAKLASQVVFKGSTTIVLPPSGNYEKLQTA 137
Qy 59 IALDVTNAYVYGYRAGNSAYFFHPDNQDAEAITHLFTDVQNYTFAGFGNYDRLEQLAG 118 Db 63 MAIDVTNAYVYGYRAGNSAYFFHPDNQDAEAITHLFTDVQNYTFAGFGNYDRLEQLAG 119	Qy 118 GNLRENIELGNGPFEIASLYYYSTGGTQLPTLARSFLICIONISEARFOYIEGEMRT 177 Db 138 GKIREXIPGPALDSATTTLFRYDS----TAAAAAFFLVLIQTAEASRFKYEQGIE 192
Qy 119 NIRENIELGNGPFEIASLYYYSTGGTQLPTLARSFLICIONISEARFOYIEGEMRT 178 Db 120 KIREKPLGLFGLDALSATTSIHYDS----TAAAAAFFLVLIQTTAEASRFKYEQGIE 174	Qy 178 RIRYNR 183 Db 193 RISKNO 198
Qy 179 IRYN 182 Db 175 IFKN 178	RESULT 15 PD0018 mistletoe lectin I A chain - Viscum album (Fragment) C; Species: Viscum album C; Date: 03-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 26-Aug-1999 C; Accession: PD0018 R; Eschenburg, S.; Krauspenhaar, R.; Mikhailov, A.; Stoeva, S.; Betzel, C.; Voelter, W. Biochem. Biophys. Res Commun. 247, 367-372, 1998 A; Title: Primary structure and molecular modeling of mistletoe lectin I from Viscum album A; Reference number: PMID:9642133 A; Accession: PD0018; MUID:98308123; PMID:9642133 A; Molecule type: protein A; Residues: 1-254 <BSC> C; Superfamily: ricin; rRNA N-glycosidase homology F; 7-246/Domain: rRNA N-glycosidase homology <RNG>
Qy 121 TAGATVQSYTINPIRAV 28.7%; Score 272.5; DB 2; Length 254; Matches 79; Best Local Similarity 37.8%; Pred. No. 1.1e-17; Mismatches 30; Indels 47; Gaps 10;	Query Match 28.7%; Score 272.5; DB 2; Length 254; Matches 79; Best Local Similarity 37.8%; Pred. No. 1.1e-17; Mismatches 30; Indels 47; Gaps 10;
Qy 122 TGTTCGEGYFRFTRITLIRDYVSGSFSENEIPIURQSTPVSADQRFLIVELTNQGQUSVA 68 Db 9 ALDVTNAYVYGYRAGNSAYFFHPDNQDAEAITHLFTDVQNYTFAGFGNYDRLEQAGN 119 Db 60 ALDVTNAYVYGYRAGNSAYFFHPDNQDAEAITHLFTDVQNYTFAGFGNYDRLEQAGN 119 Db 69 ALDVTNAYVYQAOGDSYFL-DAPRGAE-THLFTGT-TRSSLPGNSPDLENYGAH 124	Qy 123 TAGATVQSYTINPIRAV-----GRFLTNRGL-----PIN-QRFLIVELSNHAELSV 59 Db 9 THQTTCGEGYFRFTRITLIRDYVSGSFSENEIPIURQSTPVSADQRFLIVELTNQGQUSVA 68
Qy 124 IRENTIELGNGPFEIASLYYYSTGGTQLPTLARSFLICIONISEARF-----QYI 171 Db 125 -RDQIPUDLQLIQSVTALRF -- PGGSTTRQARSILLQNMISEARFNPLILWRYRQYI 180	Qy 120 IRENTIELGNGPFEIASLYYYSTGGTQLPTLARSFLICIONISEARF-----QYI 171 Db 125 -RDQIPUDLQLIQSVTALRF -- PGGSTTRQARSILLQNMISEARFNPLILWRYRQYI 180
Qy 126 E-----GEMRTRIYN 182 Db 181 NSGASFLLPDVYMLTELETSGWOOSTQYQHS 209	Search completed: February 10, 2004, 16:28:03 Job time : 11.0111 secs

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OM protein - protein search, using sw model

Run on: February 10, 2004, 16:13:55 ; Search time 6.17124 Seconds  
(without alignments)  
1409.756 Million cell updates/sec

Title: US-10-083-336A-9

Perfect score: 951  
Sequence: 1 IFPKQYDINFTTAGATVQS.....ARFOYIEGEMTRIYRNRS 185

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	934.5	RICCI_RICCO	576	1	P02879	ricinus com
2	845	AGGL_RICCO	564	1	P06750	ricinus com
3	337.5	RIPF_TRIKI	289	1	P09989	trichosanth
4	327.5	RIPS_TRIKI	289	1	P24478	trichosanth
5	327.5	ABRC_ABRR	562	1	P28590	abrus preca
6	316.5	ABRC_ABRR	527	1	P06077	abrus preca
7	312	RIP2_BRYDI	282	1	P98184	bryonia dio
8	306	RIP2_BRYDI	282	1	P31183	sambucus ni
9	300.5	RIP1_BRYDI	290	1	P31185	bryonia dio
10	291	RIBA_ABRR	258	1	P11140	abrus preca
11	290	RIPB_LUFECY	250	1	P22851	luffa cylind
12	283	RIP1_CUCFI	29	8	Q9frx4	cucumis fr
13	276	RIP1_LUFCY	277	1	P00465	luffa cylind
14	272.5	MLA_VISAL	254	1	P81446	viscum albu
15	270.5	RIP1_MOMCH	286	1	P16094	momordica c
16	268.5	RIP2_MOMBA	286	1	P29339	momordica b
17	253.5	RIP1_TRIKAN	294	1	P56626	trichosanth
18	239	RIPG_GELMU	316	1	P33186	gelonium mu
19	184	RIPA_PHYAM	294	1	P04464	phytolacca
20	177.5	RIPP_MIRJA	278	1	P21326	mirabilis j
21	168.5	RIP1_PHYAM	313	1	P10397	phytolacca
22	167	RIP2_PHYAM	261	1	P23339	phytolacca
23	131.5	RIP7_SAOF	253	1	Q41391	saponaria o
24	127.5	RIP5_SAOF	253	1	Q41389	saponaria o
25	125.5	RIP2_PHYAM	310	1	P04072	phytolacca
26	124.5	RIP6_SAOF	299	1	P20556	saponaria o
27	124	RIP0_DIACA	293	1	P24476	dianthus ca
28	121.5	RIP2_SAOF	292	1	P27559	saponaria o
29	115.5	RIP2_HORVU	280	1	P04399	hordeum vul
30	110	RIP3_SAOF	236	1	P27560	saponaria o
31	109.5	SITA_BP933	319	1	P09385	bacterioph
32	108.5	RIP1_HORVU	280	1	P22244	hordeum vul
33	100	RIP3_MAIZE	637	1	P25831	zea maya

"Ricin." Toxicon. 39:1723-1728 (2001).

[8] X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS). MEDLINE=87156983; PubMed=355197; Katzin B., Monfort W., Villafranca J.E., Monzingo A.F., Ernst S.R., Katzin B., Rutherford E., Xuong N.H., Hamlin R., Robertus J.D.; "The three-dimensional structure of ricin at 2.8 Å." J. Biol. Chem. 262:5398-5403 (1987).

[9] X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN. MEDLINE=91352004; PubMed=1881881; Katzin B.J., Collins E.J., Robertus J.D.; "Structure of ricin A-chain at 2.5 Å." Proteins 10:251-259 (1991).

[10] X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF B-CHAIN. MEDLINE=91352005; PubMed=1881882; Rutherford E., Robertus J.D.; "Structure of ricin B-chain at 2.5-Å resolution." Proteins 10:260-269 (1991).

[11] X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF A-CHAIN. MEDLINE=95082010; PubMed=990130; Weston S.A., Tucker A.D., Thatcher D.R., Derbyshire D.J., Paupitz R.A.; "X-ray structure of recombinant ricin A-chain at 1.8-Å resolution." J. Mol. Biol. 244:410-422 (1994).

[12] X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF MUTANT HIS-215. MEDLINE=96374222; PubMed=87180513; Day P.J., Ernst S.R., Franken A.F., Monzingo A.F., Pascal J.M., Molina-Svintich M.C., Robertus J.D.; "Structure and activity of an active site substitution of ricin A chain." Biochemistry 35:11098-11103 (1996).

[13] X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN. MEDLINE=97240820; PubMed=9086280; Yan X., Hollis T., Svintich M., Day P., Monzingo A.F., Milne G.W., Robertus J.D.; "Structure-based identification of a ricin inhibitor." J. Mol. Biol. 266:1043-1049 (1997).

[14] MUTAGENESIS. MEDLINE=93165632; PubMed=1287657; Xin Y., Robertus J.D.; "Analysis of several key active site residues of ricin A chain by mutagenesis and X-ray crystallography." Protein Eng. 5:775-779 (1992).

-!- FUNCTION: Ricin is highly toxic to animal cells and to a less extent to plant cells. The A chain is responsible for inhibiting protein synthesis through the catalytic inactivation of 60S ribosomal subunits. It acts as a glycosidase that removes a specific adenine residue from an exposed loop of 28S ribosomal RNA. As this loop is involved in the binding of elongation factors, the modified ribosomes are unable to support protein synthesis. The A chain can inactivate a few thousand ribosomes per minute, thus inactivating them faster than the cell can make new ones. A single A-chain molecule can therefore kill an animal cell. The B chain binds to cell receptors and facilitates the entry into the cell of the A chain. B chains are also responsible for cell agglutination (lectin activity). It binds to beta-D-galactopyranoside moieties.

-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at o-specific adenosine on the 28S rRNA.

-!- SUBUNIT: Disulfide-linked dimer of A and B chains.

-!- DOMAIN: The B chain is composed of two domains, each domain consists of 3 homologous subdomains (alpha, beta, gamma).

-!- PTM: THE MAJOR A-CHAIN IS GLYCOSYLATED ONLY IN POSITION 45 AND THE MINOR A-CHAIN IS GLYCOSYLATED ALSO IN POSITION 271.

-!- SIMILARITY: IN THE N-TERMINAL SECTION BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY TYPE 2 RTP SURTRAMITY

Query Match Score 98.3%; Pred. No. 6.9e-80; Length 576;  
 Best Local Similarity 93.4%; Conservative 0; Mismatches 0; Indels 13; Gaps 1;  
 Matches 185; -

QY 1 ITPKQPTINFTAGATVQSYNTFIAVRGRT-----NRVGLPINDRFLV 47  
 Db 36 ITPKQPTINFTAGATVQSYNTFIAVRGRTGADVRHETPVLENRGLDINQRFLV 95

QY 48 ELSNHAEVLSDVTALDVNTNAYVGYRAGNSAYFHPDNOEDAFAITHLFTDVQRYTFAFG 107  
 Db 96 ELSNHAEVLSDVTALDVNTNAYVGYRAGNSAYFHPDNOEDAFAITHLFTDVQRYTFAFG 155

QY 108 GNYDRLELAGNRLNENELGNPPLERASALVYYSTGTOLPTLARSFLICQMSAAR 167  
 Db 156 GNYDRLELAGNRLNENELGNPPLERASALVYYSTGTOLPTLARSFLICQMSAAR 215

QY 168 FQTEGENRTRIYNRSS 185  
 Db 216 FQTEGENRTRIYNRSS 233

RESULT 2  
 AC P06750;  
 ID AGGL\_RICCO  
 AC P06750;  
 ID AGGL\_RICCO  
 STANDARD; PRT; 564 AA.  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 01-JAN-1988 (Rel. 06, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Agglutinin precursor (RCA) [Contains: Agglutinin A chain (rRNA N-  
 DE Glycosidase) (EC 3.2.2.22); Agglutinin B chain].  
 OS Ricinus communis (Castor bean).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids I; Malpighiales; Euphorbiaceae; Ricinus.  
 OX NCBI\_TaxID=3988;  
 RN [1] SEQUENCE FROM N.A.  
 RP MEDLINE-0259449; PubMed=2999130;  
 RA Roberts L.M., Lamb F.J., Pappin D.J.C., Lord J.M.;  
 RT "The primary sequence of Ricinus communis agglutinin. Comparison with  
 ricin.";  
 RL J. Biol. Chem. 260:15682-15686 (1985).  
 [2] SEQUENCE OF 303-564.  
 RP TISSUE=seed;  
 RA Araki T., Yoshioka Y., Funatsu G.;  
 RT "The complete amino acid sequence of the B-chain of the Ricinus  
 communis agglutinin isolated from large-grain castor bean seeds.";  
 RL Biochim. Biophys. Acta 872:277-285(1986).

RP SEQUENCE OF 303-337.  
 RX MEDLINE-80178723; PubMed=6768555;

RA Lin T.-T.-S., Li S.-S.-L.;  
 RT "Purification and physicochemical properties of ricins and  
 agglutinins from Ricinus communis";  
 RL Eur. J. Biochem. 105:453-459(1980).

CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one  
 specific adenose on the 28S rRNA.

CC -!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-  
 INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.

CC -!- SIMILARITY: Contains 2 ricin B-type lectin domains.

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DR EMBL; M12889; AAA3369.1; -.  
 DR EMBL; S40368; AAB22584.1; -.

DR PIR; A24261; RLCSAG.  
 DR HSSP; P02879; 1BR6.  
 DR InterPro; IPR000772; Ricin\_B\_lectin.  
 DR InterPro; IPR001574; RIP.  
 DR Pfam; PF00652; Ricin\_B\_lectin; 6.  
 DR PRINTS; PR00396; SHIGARICIN.  
 DR SMART; SM0458; RICIN; 2.  
 DR PROSITE; PS50231; RICIN\_B\_LECTIN; 2.  
 DR PROSITE; PS00275; SHIGA\_RICIN; 1.  
 KW Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat;  
 KW Glycoprotein; Lectin; Signal.

FT SIGNAL; 1 24 POTENTIAL.  
 FT CHAIN; 25 290 AGGLUTININ A CHAIN.  
 FT PROPEP; 291 302 LINKER PEPTIDE.  
 FT CHAIN; 303 564 AGGLUTININ B CHAIN.  
 FT DOMAIN; 309 436 RICIN B-TYPE LECTIN 1.  
 FT DOMAIN; 439 563 RICIN B-TYPE LECTIN 2.  
 FT REPEAT; 319 361 1-ALPHA.  
 FT REPEAT; 362 402 1-BETA.  
 FT REPEAT; 405 437 1-GAMMA.  
 FT REPEAT; 450 485 2-ALPHA.  
 FT REPEAT; 489 528 2-BETA.  
 FT REPEAT; 531 558 2-GAMMA.  
 FT ACT SITE; 200 BY SIMILARITY.  
 FT DISTILLED; 282 INTERCHAIN (BY SIMILARITY).  
 FT DISULFID; 322 341 BY SIMILARITY.  
 FT DISULFID; 365 382 BY SIMILARITY.  
 FT DISULFID; 453 466 BY SIMILARITY.  
 FT DISULFID; 492 509 BY SIMILARITY.  
 FT CARBOHYD; 34 34 (POTENTIAL).  
 FT CARBOHYD; 259 N-LINKED (GLCNAC. . .).  
 FT CARBOHYD; 397 397 N-LINKED (GLCNAC. . .).  
 FT CARBOHYD; 437 437 N-LINKED (GLCNAC. . .).  
 FT CONFLICT; 331 F -> T (IN REF. 2).  
 FT CONFLICT; 362 N -> D (IN REF. 2).  
 FT CONFLICT; 374 R -> G (IN REF. 2).  
 FT CONFLICT; 404 R -> V (IN REF. 2).  
 FT CONFLICT; 552 552 RQ SEQUENCE 564 AA; 62851 MW; D455FFA72F609759 CRC64;  
 SQ Score 845; DB 1; Length 564;  
 Best Local Similarity 88.9%; Score 845; DB 1;  
 Matches 169; Conservative 85.4%; Pred. No. 1.6e-71; Indels 14; Gaps 2;

QY 1 IFPKQPTINFTAGATVQSYNTFIAVRGRT-----NRVGLPINDRFLV 47  
 Db 25 IFPKQPTINFTAGATVQSYNTFIAVRGRTGADVRHETPVLENRGLDINQRFLV 84

QY 48 ELSNHAEVLSDVTALDVNTNAYVGYRAGNSAYFHPDNOEDAFAITHLFTDVQRYTFAG 107  
 Db 85 ELSNHAEVLSDVTALDVNTNAYVGYRAGNSAYFHPDNOEDAFAITHLFTDVQNSFTFAG 144

QY 108 GNYDRLEGAGNRLNENELGNPPLERASALVYYSTGTOLPTLARSFLICQMSAAR 167  
 Db 145 GNYDRLEG-Q-GERENITLGPLEDAASALVYYSTCTQIPPLARSFLICQMSAAR 203

QY 168 FQTEGENRTRIYNRSS 185  
 Db 204 FQTEGENRTRIYNRSS 221

RESULT 3  
 ID RIPT\_TRIKI  
 ID RIPT\_TRIKI STANDARD;  
 AC P09889;  
 DT 01-NAR-1989 (Rel. 10, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ribosome-inactivating protein alpha-ribosinthin precursor  
 DE (rRNA N-Glycosidase) (EC 3.2.2.22) (Alpha-TCS)  
 OS Trichosanthes kirilowii (Mongolian snake-gourd).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; euicots; core eudicots; Rosidae;  
 OC euicots I; Cucurbitales; Cucurbitaceae; Trichosanthus .  
 RN [1] SEQUENCE FROM N.A.  
 RP STRAIN=Maximowicz; PubMed=1939291;  
 RX MEDLINE=91153657; PubMed=1939291;  
 RA Shaw P.C., Yung M.H., Zhu R.H., Ho W.K.K., Ng T.B., Yeung H.W.i.  
 RT coli.;  
 RL Gene 97:267-272(1991).  
 RN [2] SEQUENCE FROM N.A.  
 RP STRAIN=Maximowicz; TISSUE=Lesion;  
 RX MEDLINE=90256789; PubMed=2341400;  
 RA Chow T., Feldman R.A., Lovett M., Piatak M.;  
 RT Collins E.J., Robertus J.D., Lopresti M., Stone K.L., Williams K.R.,  
 RT "Isolation and DNA sequence of a gene encoding alpha-trichosanthin, a  
 RT type I ribosome-inactivating protein.";  
 RL J. Biol. Chem. 265:8670-8674(1990).  
 RN [3] SEQUENCE OF 24-270.  
 RC STRAIN=Maximowicz; TISSUE=Tuberous root;  
 RX MEDLINE=90256789; PubMed=2341399;  
 RA Wu P., Hwang K., Piatak M.;  
 RT RT models for abrin A-chain and alpha-trichosanthin.";  
 RL J. Biol. Chem. 265:8665-8669(1990).  
 RN [4] SEQUENCE OF 24-270.  
 RC TISSUE=Tuberous root;  
 RA Wang Y., Qian R.Q., Gu Z.W., Jin S.W., Zhang L.Q., Xia Z.X.,  
 RA Tian G.Y., Ni C.Z.;  
 RT "Scientific evaluation of Tian Hua Fen (THF): history, chemistry and  
 RT application.";  
 RL Pure Appl. Chem. 58:789-798(1986).  
 RN [5] X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).  
 RX MEDLINE=93344957; PubMed=3066385;  
 RA Zhou F., Fu Z., Chen M., Lin Y., Pan K.;  
 RT RT "Structure of trichosanthin at 1.88-A resolution.";  
 RL Proteins 19:4-13(1994).  
 RN [6] X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).  
 RX MEDLINE=95344383; PubMed=1619070;  
 RA Huang Q., Liu S., Tang Y., Jin S., Wang Y.;  
 RT RT "Studies on crystal structures-active-centre geometry and  
 depurinating mechanism of two ribosome-inactivating proteins.";  
 RL Biochem. J. 309:285-298(1995).  
 CC :- FUNCTION: TRICHOSANTHIN IS AN ABORTION-INDUCING PROTEIN. IT IS  
 CC CAPABLE OF INHIBITING HIV-1 INFECTION AND REPLICATION. IT  
 CC INACTIVATES EUKARYOTIC 60S RIBOSOMAL SUBUNITS.  
 CC :- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one  
 CC specific adenine on the 28S rRNA.  
 CC :- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 CC TYPE 1 RIP SUBFAMILY.

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DR EMBL; M34858; AAA34207.1; -.  
 DR PIR; J05434; AAA34206.1; -.  
 DR PDB; JTM0566; R1T2Z.  
 DR PDB; IMRKJ; 07-FEB-95.  
 DR PDB; 1TCF; 07-FEB-95.  
 DR PDB; 1TCFS; 10-JUL-95.  
 DR PDB; 1U4G; 28-JAN-03.

DR	PDB; INILI; 21-JAN-03.
	PDB; IOD2; 24-APR-00.
	DR InterPro; IPR001574; RIP.
	DR PF00161; RIP; 1.
	DR PRINTS; PR00396; SHIGARICIN.
	DR PROSITE; PS00275; SHIGARICIN; 1.
	KW Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
	KW Toxin; Signal; 3D structure.
RN	FT SIGNAL 1 23
	FT CHAIN 24 270
	FT PROPEP 271 289
	FT ACT SITE 183 183
	FT CONFLICT 57 60
	FT CONFLICT 82 84
	FT CONFLICT 87 87
	FT CONFLICT 92 92
	FT CONFLICT 143 144
	FT CONFLICT 196 196
	FT CONFLICT 215 216
	FT CONFLICT 231 231
	FT CONFLICT 234 234
	FT CONFLICT 246 266
	FT CONFLICT 247 247
	FT STRAND 25 28
	FT TURN 30 31
	FT HELIX 34 46
	FT TURN 47 47
	FT STRAND 50 54
	FT TURN 55 56
	FT STRAND 57 60
	FT HELIX 66 69
	FT STRAND 70 76
	FT TURN 78 79
	FT STRAND 82 88
	FT TURN 89 92
	FT STRAND 93 99
	FT TURN 100 101
	FT STRAND 102 105
	FT HELIX 109 114
	FT TURN 115 117
	FT STRAND 120 121
	FT TURN 124 127
	FT STRAND 134 141
	FT TURN 142 142
	FT HELIX 145 147
	FT STRAND 150 150
	FT HELIX 152 163
	FT TURN 164 165
	FT HELIX 167 180
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	FT HELIX 182 186
	FT STRAND 187 187
	FT HELIX 188 195
	FT TURN 196 196
	FT STRAND 202 202
	FT HELIX 206 226
	FT TURN 227 230
	FT STRAND 231 239
	FT TURN 241 242
	FT STRAND 245 250
	FT TURN 251 252
	FT HELIX 254 258
	FT TURN 259 259
	FT STRAND 260 263
	FT TURN 266 268
SQ	SEQUENCE 289 AA; 31676 MW; 5CE09BB630575BB9 CRC64;

Query Match 35.5%; Score 337.5; DB 1; Length 289;  
 Best Local Similarity 39.0%; Pred. No. 2.2e-24;  
 Matches 71; Conservative 42; Mismatches 50; Indels 19; Gaps 4;

9	INFTAGATVQSYTNTFIRAVRGRIN-----RVGLPINOQRFILVELSNHABLSVT	58
:::	::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::	
25	VSEFLSGATSSSSYGVFISMLRKALPERKLYDIPILRSSLPGSQRYALIHLTNYADETIS	84
59	LALDVNTNAYVGVRGNSAXFFHPDNOEDA-EAITHLFTDVQNRYTFAFGGNYDRDEQLA	117
::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::		
85	VAVDVNTVYIMGTRGDSYFF---NEASATEAAKVFKDAMRKTLPVSYNERQYQTA	141
118	GNLRENIELNGNGLPEAISALYYSTGGTOLPLTARSFEIICQIMSEAAFRQYIEGEMRT	177
::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::		
142	GKIRENTIPLGLPAIDSAITLFYNNAN----SAASALMVLIOSTSSEAAFRKFIEQQIGK	196
178	RI 179	
::   ::		
197	RV 198	
SWISS-PROT_4		
PS_TRIKI	STANDARD;	PRT; 289 AA.
RIPS_TRIKI		
P24478;		
01-MAR-1992 (Rel. 21, Created)		
15-DEC-1998 (Rel. 37, Last sequence update)		
28-FEB-2003 (Rel. 41, Last annotation update)		
Ribosome-inactivating protein karasurin precursor (rRNA		
N-glycosidase) (EC 3.2.2.22).		
Trichosanthes kirilowii (Mongolian snake-gourd).		
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;		
eucommiales; I; Cucurbitales; Cucurbitaceae; Trichosanthes.		
NCBI_TAXID=3677;		
[1]		
SEQUENCE FROM N.A.		
TISSUE=Root tuber;		
MEDLINE:9735662; PubMed:9212998;		
Mizukami H., Iida K., Kondo T., Ogihara Y.;		
"Cloning and bacterial expression of a gene encoding ribosome-		
inactivating proteins, karasurin-A and karasurin-C, from Trichosanthes		
kirilowii var. japonica";		
Biol. Pharm. Bull. 20:711-713 (1997).		
[2]		
SEQUENCE OF 24-270.		
MEDLINE:92005521; PubMed:1914000;		
Toyokawa S., Takeda T., Kato Y., Wakabayashi K., Ogihara Y.;		
"The complete amino acid sequence of an abortifacient protein,		
karasurin.";		
Chem. Pharm. Bull. 39:1244-1249 (1991).		
-1- FUNCTION: ABORTION-INDUCING PROTEIN. IT INACTIVATES EUKARYOTIC		
60S RIBOSOMAL SUBUNITS.		
-1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one		
specific adenine on the 28S rRNA.		
-1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.		
TYPE 1 RIP SUBFAMILY.		
-----		
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the European Bioinformatics Institute. There are no restrictions on its		
use by non-profit institutions as long as its content is in no way		
modified and this statement is not removed. Usage by and for commercial		
entities requires a license agreement (See <a href="http://www.ebi.ac.uk/announce/">http://www.ebi.ac.uk/announce/</a>		
or send an email to <a href="mailto:license@ebi.ac.uk">license@ebi.ac.uk</a> ).		
EMBL; AB00666; BAA21786.1; - .		
PIR; JC5606; JCS606.		
PIRA; JT0333; JT0393.		
HSSP; P09889; 1MRJ.		
InterPro; IPR01574; RIP.		
Pfam; PF00161; RIP; 1.		
PRINTS; PRO0396; SHIGARICIN.		
PROSITE; PS00275; SHIGA_RICIN; 1.		
Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;		
Toxin; Signal.		
SIGNAL; 1		
POTENTIAL; 21		

FT	CHAIN	22	270	KARASURIN-C.
FT	CHAIN	24	270	KARASURIN-N.A.
FT	PROPEP	271	289	REMOVED IN NATURE FORM.
FT	ACT SITE	183	183	BY SIMILARITY.
SQ	SEQUENCE	289 AA;	31704 MW;	883D3E3242887B26 CRC64;
Query Match	9	INFITAGATVQSYTNTFIRAVGRGLTN-	-----	-RVGLPINRFLIVELNSNFAELSVY-
Best Local Similarity	34.4%	Score 327.5;	DB 1;	Length 289;
Matches	71	VSFRISGATSSSFGVFSNLKAPYERKLYDPILLRSTLPGSQRYALIHLTYADETIS	50;	Indels 19; Gaps
Qy		:   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :		
Db	25	LADDTYNAYVGTRAGNSAYFFHDNOEDA-EAITHLEFDVONRYTFAGFGNYDRLEOA		
Qy	59	GNDTNTYVYGVTRAGDTSYFF--NEASATEAKYVFKAKRKVTLPSGNYERLQIAA		
Db	85	VAIDVTNTYVNGTRAGDTSYFF--		
Qy	118	GNLRENIEIENGPLEEAISALYYXSTGGTOLPLARSFCIOMISEAARFYQLEGEMET		
Db	142	GKIRENIPLGPLAUDSATTLTYFVNAN---SAASALMVLQISTSEARYKFEEQICK		
Qy	178	RI 179		
Db	197	RV 198		
<b>RESULT 5</b>				
<b>ABRC_ABRPR</b>				
ID	ABRC_ABRPR	STANDARD:	PRT:	562 AA.
AC	P28550;			
DT	01-DBC-1992 (Rel. 24, Created)			
DT	01-DBC-1992 (Rel. 24, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Abrin-c A chain [Contains: Abrin-c A chain (rRNA N-glycosidase)]			
DE	(EC 3.2.2.22); Abrin-c B chain [Contains: Abrin-c B chain (rRNA N-glycosidase)]			
OS	<i>Abrus precatorius</i> (Indian licorice) (Crab's eye).			
OC	Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicots; core eudicots; Rosidae;			
OC	eurosid I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.			
OX	NCBI_TaxID:3816;			
RN	SEQUENCE FROM N.A.			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Leaf;			
RX	Medline=91266957; PubMed=2050149;			
RA	Wood K.A., Lord J.M., Wawrzynczak E.J., Piatak M.;			
RT	"Preproabrin: genomic cloning, characterisation and the expression of the A-chain in <i>Escherichia coli</i> ";			
RT	Eur. J. Biochem. 198:723-732 (1991).			
RL				
CC	-!- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RNA. THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT BELONGS TO THE B-CHAIN SUPERFAMILY. IT IS COMPOSED OF TWO DOMAINS EACH DOMAIN CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).			
CC	-!- SIMILARITY: IN THE N-TERMINAL SECTION, BELONGS TO THE RIBOSOME-1 INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.			
CC	-!- SIMILARITY: Contains 2 ricin B-type lectin domains.			
CC	This SWISS-PROT entry is oprotein. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce.html">http://www.isb-sib.ch/announce.html</a> or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> .			
CC	EMBL: X55667; CAA39302.1; -			
CC	PIR: S16022; S16022.			
CC	DR DR			

MEDLINE=93132798; PubMed=8421313; Hung C.-H., Lee M.-C., Lee T.-C., Lin J.-Y.; "Primary structure of three distinct isoabrinins determined by cDNA sequencing. Conservation and significance."; J. Mol. Biol. 229:263-267 (1993). [2]	SEQUENCE OF 260-527. TDSINE=Seed; MEDLINE=91169023; PubMed=7763422; Kimura M., Sumizawa T., Funatsu G.; "The complete amino acid sequences of the B-chains of abrin-a and abrin-b, toxic proteins from the seeds of Abrus precatorius."; Biotechnol. Biochem. 57:166-169 (1993). -!- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RNA. ABRIN-A IS MORE TOXIC THAN RICIN. -!- FUNCTION: THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT FACILITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT PRECEDES ENDOCYTOSIS. -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at specific adenosine on the 28S rRNA. -!- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS. -!- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA). -!- SIMILARITY: IN THE N-TERMINAL SECTION: BELONGS TO THE RIBOSOME INACTIVATING PROTEIN FAMILY. TYPE RIP SUPERFAMILY. -!- SIMILARITY: Contains 2 ricin B-type lectin domains.
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	EMBL; M98345; AAA32625; 1; -. PIR; S22430; S32430. HSSP; P1140; IABR. InterPro; IPR00072; Ricin_B_lectin. InterPro; IPR001574; RIP. PFAM; PF00652; Ricin_B_lectin; 6. PRINTS; PR00396; SHIGARICTM. SMART; SM00458; RICIN. PROSITE; PS05231; RICIN_B_LECTIN; 2. PROSITE; PS00275; SHIGA_RICIN; 1. Plant defensin; Hydrolase; Protein synthesis inhibitor; Toxin; Repetition domain; Glycoprotein; Lectin; Pyrrolidone carboxylic acid. CHAIN 1 250 ABRIN-B A CHAIN. LINKER PEPTIDE. ABRIN-B B CHAIN. CHAIN 261 527 ABRIN-B B CHAIN. REPEAT 272 399 RICIN B-TYPE LECTIN 1. DOMAIN 402 526 RICIN B-TYPE LECTIN 2. REPEAT 402 526 1-ALPHA. REPEAT 282 324 1-BETA. REPEAT 325 365 1-GAMMA. REPEAT 368 400 2-ALPHA. REPEAT 413 448 2-BETA. REPEAT 452 491 2-GAMMA. REPEAT 494 527 2-GAMMA. ACT SITE 163 163 BY SIMILARITY. DISULFID 246 268 INTERCHAIN (BY SIMILARITY). DISULFID 285 304 BY SIMILARITY. DISULFID 328 345 BY SIMILARITY. DISULFID 416 429 BY SIMILARITY. DISULFID 455 472 BY SIMILARITY. MOD. RES 1 1 PYRROLIDONE CARBOXYLIC ACID (BY SIMILARITY). N-LINKED (GLCNAC. . .) (POTENTIAL). N-LINKED (GLCNAC. . .) (POTENTIAL). N-LINKED (GLCNAC. . .) (POTENTIAL). N-> D (IN REF. 2).
CARBOHYD	110 110 CARBOHYD 360 360 CARBOHYD 400 400 CARBOHYD 282 282

D T 291 C91 D -> N (IN REF. 2).  
 T T 350 351 AE -> PQ (IN REF. 2).  
 CONFLICT S -> N (IN REF. 2).  
 T T 378 378 S -> N (IN REF. 2).  
 CONFLICT 426 426 L -> M (IN REF. 2).  
 T T 428 428 Y -> D (IN REF. 2).  
 CONFLICT 428 428 N -> S (IN REF. 2).  
 T T 431 431 R -> K (IN REF. 2).  
 CONFLICT 484 484 N -> S (IN REF. 2).  
 T T 491 491 H -> Y (IN REF. 2).  
 CONFLICT 493 493 R -> G (IN REF. 2).  
 T T 502 502 E -> Q (IN REF. 2).  
 CONFLICT 509 509 H -> W (IN REF. 2).  
 T T 513 513 H -> T (IN REF. 2).  
 CONFLICT 516 516 H -> W (IN REF. 2).  
 T T 527 AA: 59114 MW: 3253.8E+90CE89494A CRC64;  
 SEQUENCE  
 Query Match 33.3%; Score 316.5; DB 1; Length 527;  
 Best Local Similarity 42.9%; Pred. No. 4. 3e-22;  
 Matches 81; Conservative 23; Mismatches 66; Indels 19; Gaps 5;  
 Matches 81;  
 5 QYPLINFPTAGATVQSYNTNFIRAVGRGLTNRV--GLPI-----NORFILVELSNHEA 53  
 1 QDQVKTPTEGATQSQSYKQFIEALQRQLTGGLINGPVLDPPTLQLERRYTISVLSNSD 60  
 54 ELSVTLADLVINAVGFRAGNSAIFTFHQNQDEAITHFLDQYRITYFAFGCNYDR 113  
 61 TSEAGIDVSNAVVAIRAGNRSYFL--RDAPTSASVYLFTGQ-OXLRFLRGNSYIDL 116  
 114 EOLAGNLRNENIEGLNGPLEEAISALYYSTGGTGTOLPLTLSFIIQOMTSEAARFOYIEG 173  
 117 ERLARQTROQIPLGLQALKHAFSL---QSGTDDQEIARTLIVIQMSEANTRFISY 172  
 Dy 174 EMRTRIYRN 182  
 Db 173 RGVSVRTN 181

**RESULT<sup>7</sup>**  
 RIP2\_BRYDI\_RIP2\_BRYDI STANDARD; PRT; 282 AA.  
 AC P98184; Q9S8J0;  
 DT 16-OCT-2001 (Rel. 4.0, Created)  
 DT 16-OCT-2001 (Rel. 4.0, Last sequence update)  
 DT 28-FEB-2003 (Rel. 4.1, Last annotation update)  
 DE Ribosome-inactivating protein bryodin II precursor (rRNA N-glycosidase) (EC 3.2.2.22) (BU2).  
 OS Bryonia dioica (Red bryony).  
 OX Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; Rosidae; euroids I; Cucurbitales; Cucurbitaceae; Bryonia. NCBI\_TaxID=36532;  
 RN [1] SEQUENCE FROM N.A.  
 RA Siegall C.B., Gawlik S.L., Marquardt H.;  
 RA "Bryodin 2 a ribosome-inactivating protein isolated from the plant  
 RT Bryonia dioica";  
 RL Patent number US5597569, 28-JAN-1997.  
 RN [2] SEQUENCE OF 22-42.  
 RC TISSUE=Root;  
 RX MEDLINE=95151812; PubMed=7849072;  
 RA Siegall C.B., Gawlik S.L., Chace D., Wolff E.A., Mixan B., Marquardt H.;  
 RA "Characterization of ribosome-inactivating proteins isolated from  
 RT Bryonia dioica and their utility as carcinoma-reactive  
 RT immunoconjugates.,";  
 RL Bioconj. Chem. 5:423-429 (1994).  
 CC [-] FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1, INHIBITS  
 CC PROTEIN SYNTHESIS IN ANIMAL CELLS (BY SIMILARITY).  
 CC [-] CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one  
 CC specific adenine on the 28S rRNA.  
 CC [-] SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 CC TYPE 1 RIP SUBFAMILY

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EMBL; I34238; -; NOT_ANNOTATED_CDS.	
HSSP; P09898; 1MRJ.	
InterPro; IPR001574; RIP.	
DR Pfam; PF00161; RIP_1.	
DR PRINTS; PR00396; SHIGARICIN.	
DR PROSITE; PS00275; SHIGA_RICIN_1.	
DR KW PLANT defense; Protein synthesis inhibitor; Hydrolase; Toxin; Multigene family; Glycoprotein; Signal.	
DR KW SIGNAL 1 21 RIBOSOME-INACTIVATING PROTEIN BRYODIN II.	
DR ACT SITE 22 282 BY SIMILARITY.	
DR CARBOHYD 25 183 N-LINKED GLCNAc. . . (POTENTIAL).	
DR SEQUENCE 282 AA; 30754 MW; C52BE2FCA873769C CRC64;	
Query Match Score 32.8%; Best Local Similarity 45.5%; Pred. No. 5.3e-22; Length 282; Matches 81; Conservative 24; Mismatches 49; Indels 24; Gaps 8;	
Qy 9 INFETTAGATVOSYNMFIRAVRGRILTRNVG-----LPINO-----RFILVELSNHAEI 55  : :   :   :   :   :   :   :   :   :   :   :   :   :   :   : Ddb 24 INFESLIGATGATYKTFTRNLRTKL-----VGTPRVYDIPVLRNAAAGIARFLQLVTLYNGE 81	
Qy 56 SVTIALDTNAYVYGRAGNSAYFFPDNOEDAELTHLFDVQNYYTFAFGGNYDLEQ 115  :   :   :   :   :   :   :   :   :   :   :   :   :   :   : Ddb 82 SVTVIALDVYVNVYVYAGRNTAYFL--ADASSTEANVLFAGI-NEVRVLPYGGNYDGETL 137	
Qy 116 LAGVN-RENTELGNGLPEEEAISALYYSTGTQLPLARSFLICQNISEARFQYIE 172  :   :   :   :   :   :   :   :   :   :   :   :   :   : Ddb 138 AAGRISRENIELGPSEISSAIGNMFRHNP-GTSVP--RAFIVIIQTVSEARFKWIE 191	
RESULT 8	
NIGRIN SAMNI STANDARD; PRT; 563 AA.	
NIGB SAMNI STANDARD; PRT; 563 AA.	
P33183; P33184; P9542; STANDARD; PRT; 563 AA.	
AC ID TISSUE=Bark; MEDLINE=96215449; PubMed=840135; RT DT (Rel. 1-27, Created) RT DT 01-OCT-1993 (Rel. 1-41, Last sequence update) RT DT 28-FEB-2003 (Rel. 1-41, Last annotation update)	
Van Damme B.J.; Barre A.; Rouge P.; Van Leuven F.; Peumans W.J.; Iglesias R.; RT "Characterization and molecular cloning of Sambucus nigra agglutinin V chain (nigrin b), a GalNAc-specific type-2 ribosome-inactivating protein from the bark of elderberry (Sambucus nigra)." RT Eur. J. Biochem. 237:505-513 (1996). RT [2]	
NCBI TaxID=4202; RN SEQUENCE OF 26-49 AND 298-321. RT TISSUE=Bark; MEDLINE=90307; PubMed=840135; RT RX Girbau T.; Citteros L.; Ferreras J.M.; Rojo M.A.; Iglesias R.; RA Munoz R.; Arias F.J.; Calonge M.; Garcia J.R.; Mendez E.; RA "Isolation and partial characterization of nigrin b, a non-toxic novel type 2 ribosome-inactivating protein from the bark of Sambucus nigra L." RT Plant Mol. Biol. 22:1101-1106(1993). RT CC [-] FUNCTION: NON-TOXIC TYPE 2 RIP WHICH STRONGLY INHIBITS MAMMALIAN	

PROTEIN SYNTHESIS BUT DOES NOT AFFECT PLANT NOR BACTERIAL PROTEIN SYNTHESIS. THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN SUBUNITS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S rRNA. THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT FACILITATES THE BINDING OF NIGRIN B TO THE CELL MEMBRANE THAT PRECEDES ENDOCYTOSIS.

-|- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one

specific adenine on the 28S rRNA.

CC -|- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.

CC -|- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-

CC -|- INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.

CC -|- SIMILARITY: Contains 2 ricin B-type lectin domains.

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CC EMBL: U41299; AAB39475.1; -.

DR PIR; S37382; S37382.

DR InterPro; IPR000772; Ricin\_B\_lectin.

DR InterPro; IPR001574; RIP.

DR Pfam; PF00652; Ricin\_B\_lectin\_6.

DR Pfam; PF0161; RIP\_1.

DR PRINTS; PR0396; STIGARICIN.

DR SMART; SM00458; RICIN\_2.

DR PROSITE; PS00275; SHIGA\_RICIN\_1.

DR PROSITE; PS00231; RICIN; RICIN\_B\_LECVIN\_2.

DR PROSITE; PS00231; RICIN; RICIN\_B\_LECVIN\_2.

KW Plant defensin; Hydrolase; Lectin; Signal; Toxin; Repeat;

KW Glycoprotein; Lectin; Signal.

FT SIGNAL 1 25

FT CHAIN 26 297

FT CHAIN 298 563

FT DOMAIN 305 431

FT DOMAIN 434 559

FT REPEAT 316 356

FT REPEAT 357 397

FT REPEAT 400 412

FT REPEAT 445 482

FT REPEAT 486 524

FT REPEAT 527 554

FT ACT SITE 188

FT DISULFID 274

FT DISULFID 319

FT DISULFID 360

FT DISULFID 448

FT DISULFID 489

FT DISULFID 506

FT CARBOHYD 221

FT CARBOHYD 368

FT CARBOHYD 376

FT CARBOHYD 483

FT CARBOHYD 537

FT CONFLICT 39

FT SEQUENCE 563 AA;

FT DISULFID 302

FT DISULFID 338

FT DISULFID 377

FT DISULFID 463

FT DISULFID 489

FT CARBOHYD 221

FT CARBOHYD 368

FT CARBOHYD 376

FT CARBOHYD 483

FT CARBOHYD 537

FT CONFLICT 39

FT SEQUENCE 62300 MW;

FT 250CBEB24621BFL4

FT CRC64;

FT CRYSTALLOGRAPHY

FT DB 1;

FT DB 563;

FT DB 4-4e-21;

FT DB 36;

FT DB 53;

FT DB 6;

FT DB 52;

FT DB 87;

FT DB 88 NGNTVTLAVDTVNLXVVAFSGNANSYFF --- KDATEVQSNLFVGTTQN-TLSFTGNY 141

FT DB 111 DRLEQLAGNIRETELGNQPLEEAISALYYSTGGTQLPLTALSFIOLQMSAEAFQY 170

PROTEIN SYNTHESIS BUT DOES NOT AFFECT PLANT NOR BACTERIAL PROTEIN SYNTHESIS. THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN SUBUNITS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S rRNA. THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT FACILITATES THE BINDING OF NIGRIN B TO THE CELL MEMBRANE THAT PRECEDES ENDOCYTOSIS.

-|- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one

specific adenine on the 28S rRNA.

CC -|- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.

CC -|- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-

CC -|- INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.

CC -|- SIMILARITY: Contains 2 ricin B-type lectin domains.

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REVIEW 9  
R1P1\_BRVDI STANDARD; PRT; 290 AA.

AC P31185; Q8S819; 01-OCT-1993 (Rel. 27, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Ribosome-inactivating protein bryodin I Precursor (rRNA N-glycosidase) (EC 3.2.2.22) (BDI).

OS Bryonia dioica (Red bryony).

OC Viridiplantae; Streptophytai; Embryophytai; Tracheophytai.

OC Spermatophytai; Magnoliophytai; eu dicots; eudicots; Rosidae;

OC eurosid I; Cucurbitales; Cucurbitaceae; Bryonia.

NCBI\_TaxID=3652; NCBI\_TaxID=3652;

[1] RN SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).

RP TISSUE=leaf; TISSUE=leaf;

RX MEDLINE=97226081; PubMed=9115985;

RA Gawlik S.L., Neubauer M., Klei H.E., Einspahr H.M., Siegall C.B.;

RA "Molecular, biological, and preliminary structural analysis of recombinant bryodin 1, a ribosome-inactivating protein from the plant Bryonia dioica." Biochemistry 36:3095-3103 (1997).

[2] RN SEQUENCE FROM N.A.

RA Siegall C.B.; "Cloning and expression of a gene encoding bryodin 1 from Bryonia dioica."

RT Patent number US5541110, 30-JUL-1996.

[3] RN SEQUENCE OF 24-66.

RC TISSUE=Seed; MEDLINE=89326691; PubMed=2753596;

RA Montecuccchi P.C., Lazzarini A.M., Barbieri L., Stirpe F., Soria M., Lappi D.; "N-terminal sequence of some ribosome-inactivating proteins." Int. J. Pept. Protein Res. 33:263-267(1989).

[4] RN SEQUENCE OF 24-43.

RC TISSUE=Root; MEDLINE=95151812; PubMed=7849072;

RA Siegall C.B., Gawlik S.L., Chace D., Wolff E.A., Mixan B., Margardt H.; "Characterization of ribosoma-inactivating proteins isolated from Bryonia dioica and their utility as carcinoma-reactive immunconjugates." Bioconjug. Chem. 5:423-429(1994).

CC -|- FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1, INHIBITS PROTEIN SYNTHESIS IN ANIMAL CELLS.

CC -|- CATALYTIC ACTIVITY: Endohydrolase of the N-glycosidic bond at one specific adenine on the 28S rRNA.

CC -|- PIM: APPEARS TO UNDERGO PROTEOLYTIC CLEAVAGE IN THE C-TERMINAL TO PROTEIN SYNTHESIS IN ANIMAL CELLS.

CC -|- BIOTECHNOLOGY: Especially useful as immunotoxin for pharmaceutical applications as it has low toxicity in rats and mice but is potent once inside target cells.

CC -|- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.

CC -|- TYPE 1 RIP SUBFAMILY.

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REVIEW 9  
R1P1\_BRVDI STANDARD; PRT; 290 AA.

AC P31185; Q8S819; 01-OCT-1993 (Rel. 27, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Ribosome-inactivating protein bryodin I Precursor (rRNA N-glycosidase) (EC 3.2.2.22) (BDI).

OS Bryonia dioica (Red bryony).

OC Viridiplantae; Streptophytai; Embryophytai; Tracheophytai.

OC Spermatophytai; Magnoliophytai; eu dicots; eudicots; Rosidae;

OC eurosid I; Cucurbitales; Cucurbitaceae; Bryonia.

NCBI\_TaxID=3652; NCBI\_TaxID=3652;

[1] RN SEQUENCE FROM N.A.

RA Siegall C.B.; "Cloning and expression of a gene encoding bryodin 1 from Bryonia dioica."

RT Patent number US5541110, 30-JUL-1996.

[2] RN SEQUENCE OF 24-66.

RC TISSUE=Seed; MEDLINE=89326691; PubMed=2753596;

RA Montecuccchi P.C., Lazzarini A.M., Barbieri L., Stirpe F., Soria M., Lappi D.; "N-terminal sequence of some ribosome-inactivating proteins." Int. J. Pept. Protein Res. 33:263-267(1989).

[3] RN SEQUENCE OF 24-43.

RC TISSUE=Root; MEDLINE=95151812; PubMed=7849072;

RA Siegall C.B., Gawlik S.L., Chace D., Wolff E.A., Mixan B., Margardt H.; "Characterization of ribosoma-inactivating proteins isolated from Bryonia dioica and their utility as carcinoma-reactive immunconjugates." Bioconjug. Chem. 5:423-429(1994).

CC -|- FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1, INHIBITS PROTEIN SYNTHESIS IN ANIMAL CELLS.

CC -|- CATALYTIC ACTIVITY: Endohydrolase of the N-glycosidic bond at one specific adenine on the 28S rRNA.

CC -|- PIM: APPEARS TO UNDERGO PROTEOLYTIC CLEAVAGE IN THE C-TERMINAL TO PROTEIN SYNTHESIS IN ANIMAL CELLS.

CC -|- BIOTECHNOLOGY: Especially useful as immunotoxin for pharmaceutical applications as it has low toxicity in rats and mice but is potent once inside target cells.

CC -|- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.

CC -|- TYPE 1 RIP SUBFAMILY.

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REVIEW 9  
R1P1\_BRVDI STANDARD; PRT; 290 AA.

AC P31185; Q8S819; 01-OCT-1993 (Rel. 27, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Ribosome-inactivating protein bryodin I Precursor (rRNA N-glycosidase) (EC 3.2.2.22) (BDI).

OS Bryonia dioica (Red bryony).

OC Viridiplantae; Streptophytai; Embryophytai; Tracheophytai.

OC Spermatophytai; Magnoliophytai; eu dicots; eudicots; Rosidae;

OC eurosid I; Cucurbitales; Cucurbitaceae; Bryonia.

NCBI\_TaxID=3652; NCBI\_TaxID=3652;

[1] RN SEQUENCE FROM N.A.

RA Siegall C.B.; "Cloning and expression of a gene encoding bryodin 1 from Bryonia dioica."

RT Patent number US5541110, 30-JUL-1996.

[2] RN SEQUENCE OF 24-66.

RC TISSUE=Seed; MEDLINE=89326691; PubMed=2753596;

RA Montecuccchi P.C., Lazzarini A.M., Barbieri L., Stirpe F., Soria M., Lappi D.; "N-terminal sequence of some ribosome-inactivating proteins." Int. J. Pept. Protein Res. 33:263-267(1989).

[3] RN SEQUENCE OF 24-43.

RC TISSUE=Root; MEDLINE=95151812; PubMed=7849072;

RA Siegall C.B., Gawlik S.L., Chace D., Wolff E.A., Mixan B., Margardt H.; "Characterization of ribosoma-inactivating proteins isolated from Bryonia dioica and their utility as carcinoma-reactive immunconjugates." Bioconjug. Chem. 5:423-429(1994).

CC -|- FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1, INHIBITS PROTEIN SYNTHESIS IN ANIMAL CELLS.

CC -|- CATALYTIC ACTIVITY: Endohydrolase of the N-glycosidic bond at one specific adenine on the 28S rRNA.

CC -|- PIM: APPEARS TO UNDERGO PROTEOLYTIC CLEAVAGE IN THE C-TERMINAL TO PROTEIN SYNTHESIS IN ANIMAL CELLS.

CC -|- BIOTECHNOLOGY: Especially useful as immunotoxin for pharmaceutical applications as it has low toxicity in rats and mice but is potent once inside target cells.

CC -|- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.

CC -|- TYPE 1 RIP SUBFAMILY.

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REVIEW 9  
R1P1\_BRVDI STANDARD; PRT; 290 AA.

AC P31185; Q8S819; 01-OCT-1993 (Rel. 27, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Ribosome-inactivating protein bryodin I Precursor (rRNA N-glycosidase) (EC 3.2.2.22) (BDI).

OS Bryonia dioica (Red bryony).

OC Viridiplantae; Streptophytai; Embryophytai; Tracheophytai.

OC Spermatophytai; Magnoliophytai; eu dicots; eudicots; Rosidae;

OC eurosid I; Cucurbitales; Cucurbitaceae; Bryonia.

NCBI\_TaxID=3652; NCBI\_TaxID=3652;

[1] RN SEQUENCE FROM N.A.

RA Siegall C.B.; "Cloning and expression of a gene encoding bryodin 1 from Bryonia dioica."

RT Patent number US5541110, 30-JUL-1996.

[2] RN SEQUENCE OF 24-66.

RC TISSUE=Seed; MEDLINE=89326691; PubMed=2753596;

RA Montecuccchi P.C., Lazzarini A.M., Barbieri L., Stirpe F., Soria M., Lappi D.; "N-terminal sequence of some ribosome-inactivating proteins." Int. J. Pept. Protein Res. 33:263-267(1989).

[3] RN SEQUENCE OF 24-43.

RC TISSUE=Root; MEDLINE=95151812; PubMed=7849072;

RA Siegall C.B., Gawlik S.L., Chace D., Wolff E.A., Mixan B., Margardt H.; "Characterization of ribosoma-inactivating proteins isolated from Bryonia dioica and their utility as carcinoma-reactive immunconjugates." Bioconjug. Chem. 5:423-429(1994).

CC -|- FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1, INHIBITS PROTEIN SYNTHESIS IN ANIMAL CELLS.

CC -|- CATALYTIC ACTIVITY: Endohydrolase of the N-glycosidic bond at one specific adenine on the 28S rRNA.

CC -|- PIM: APPEARS TO UNDERGO PROTEOLYTIC CLEAVAGE IN THE C-TERMINAL TO PROTEIN SYNTHESIS IN ANIMAL CELLS.

CC -|- BIOTECHNOLOGY: Especially useful as immunotoxin for pharmaceutical applications as it has low toxicity in rats and mice but is potent once inside target cells.

CC -|- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.

CC -|- TYPE 1 RIP SUBFAMILY.

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CC - INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.  
 CC - I- SIMILARITY: Contains 2 ricin B-type lectin domains.

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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC or send an email to license@isb-sib.ch).

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CC EMBL; M9344; AAA32624.1; ALT INIT.  
 DR EMBL; X54872; -; NOT\_ANNOTATED\_CDS.  
 DR PIR; S52429; T2LSA.  
 DR PDB; 1ABR; 07-FEB-95.  
 DR InterPro; IPR000772; Ricin\_B\_lectin.  
 DR InterPro; IPR001574; RIP.  
 DR PFAM; PF00652; Ricin\_B\_lectin; 6.  
 DR Pfam; PF00161; RIP; 1.  
 DR SMART; SMC0458; RICIN; 2.  
 DR PROSITE; PS50231; RICIN\_BLECTIN; 2.  
 DR PROSITE; PS00275; SHIGA\_RICIN; 1.  
 KW Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat;  
 KW Glycoprotein; Lectin; 3D-structure; Pyrrolidone carboxylic acid.  
 FT CHAIN 1 ABRIN-A A CHAIN.  
 FT PEPTIDE 251 LINKER PEPTIDE.  
 FT CHAIN 262 ABRIN-A B CHAIN.  
 FT DOMAIN 273 RICIN B-TYPE LECTIN 1.  
 FT REPEAT 403 RICIN B-TYPE LECTIN 2.  
 FT REPEAT 283 325 1-ALPHA.  
 FT REPEAT 326 366 1-BETA.  
 FT REPEAT 369 401 1-GAMMA.  
 FT REPEAT 414 449 2-ALPHA.  
 FT REPEAT 492 528 2-BETA.  
 FT REPEAT 495 528 2-GAMMA.  
 FT ACT SITE 164 164 BY SIMILARITY.  
 FT DISULFID 247 269 INTERCHAIN (BY SIMILARITY).  
 FT DISULFID 286 305 BY SIMILARITY.  
 FT DISULFID 329 346 BY SIMILARITY.  
 FT DISULFID 417 430 BY SIMILARITY.  
 FT DISULFID 456 473 BY SIMILARITY.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT CARBOHYD 361 361 N-LINKED (GLCNAC. ; ).  
 FT CARBOHYD 401 401 N-LINKED (GLCNAC. ; ).  
 FT CONFLICT 202 202 MISSING (IN REF. 2).  
 FT CONFLICT 298 298 N -> Y (IN REF. 4).  
 FT CONFLICT 427 427 M -> L (IN REF. 4).  
 FT CONFLICT 467 467 T -> P (IN REF. 4).  
 FT CONFLICT 483 483 V -> L (IN REF. 4).  
 FT STRAND 5 8  
 FT TURN 10 11  
 FT HELIX 14 28  
 FT STRAND 32 33  
 FT TURN 34 35  
 FT STRAND 36 38  
 FT TURN 42 43  
 FT HELIX 47 49  
 FT STRAND 51 57  
 FT TURN 63 69  
 FT STRAND 70 72  
 FT STRAND 75 79  
 FT STRAND 83 86  
 FT TURN 88 89  
 FT HELIX 92 93  
 FT HELIX 94 97  
 FT TURN 100 101  
 FT STRAND 103 106  
 FT TURN 113 114  
 FT HELIX 115 119  
 FT TURN 124 126  
 FT STRAND 129 129  
 FT HELIX 131 131

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FT TURN 143 144  
 FT HELIX 148 167  
 FT STRAND 168 168  
 FT HELIX 169 180  
 FT STRAND 181 182  
 FT STRAND 185 185  
 FT HELIX 189 196  
 FT TURN 197 197  
 FT HELIX 198 207  
 FT STRAND 212 220  
 FT TURN 222 223  
 FT TURN 226 231  
 FT TURN 232 233  
 FT HELIX 235 239  
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 FT STRAND 243 243  
 FT HELIX 248 248  
 FT STRAND 268 268  
 FT STRAND 276 277  
 FT HELIX 279 280  
 FT HELIX 282 284  
 FT STRAND 286 289  
 FT HELIX 290 292  
 FT TURN 296 297  
 FT STRAND 299 303  
 FT HELIX 311 313  
 FT STRAND 315 317  
 FT TURN 319 320  
 FT STRAND 322 325  
 FT TURN 326 327  
 FT STRAND 328 332  
 FT TURN 337 338  
 FT STRAND 340 344  
 FT TURN 346 348  
 FT HELIX 351 353  
 FT STRAND 355 355  
 FT STRAND 357 358  
 FT TURN 360 361  
 FT STRAND 364 366  
 FT TURN 367 370  
 FT STRAND 371 374  
 FT TURN 380 381  
 FT STRAND 383 383  
 FT STRAND 385 387  
 FT HELIX 393 395  
 FT STRAND 398 399  
 FT STRAND 406 408  
 FT TURN 410 411  
 FT HELIX 413 415  
 FT STRAND 417 421  
 FT TURN 422 423  
 FT STRAND 424 428  
 FT TURN 432 433  
 FT HELIX 435 437  
 FT STRAND 437 441  
 FT TURN 443 444  
 FT STRAND 447 449  
 FT TURN 450 451  
 FT STRAND 452 459  
 FT TURN 464 465  
 FT STRAND 467 472  
 FT TURN 474 475  
 FT HELIX 478 480  
 FT STRAND 483 484  
 FT TURN 486 487  
 FT STRAND 490 492  
 FT TURN 493 496  
 FT STRAND 497 501

Query Match 30.6%; Score 291, DB 1; Length 528;  
 Best Local Similarity 40.6%; Pred. No. 1e-19; Mismatches 59; Indels 26; Gaps 7;  
 Matches 76; Conservative 26; Mismatches 59; Indels 26; Gaps 7;

9 INFITAGATVQSYTNFIRAVRGRLTNRYGL---PI-----NQFILVELSNHAEL 55  
 5 IKFSTEGATQSQSYKFIEARL---RGGLIHD.PVLPPTTLEARNYTVITVELNSDTE 62

Qy 56 SVTLADLVNTAYVGYRAGNSAYFFH---PDNEQDAEAITHLFPTDVQNRFTFAFGCGNYDRL 113  
 Db 63 SIEVGIDVTNAYVGYRAGNSAYFFH---PDNEQDAEAITHLFPTDVQNRFTFAFGCGNYDRL 116  
 Qy 114 EQLAMNIRENTIELGNGPFLPEAISALAYYYSTGGTQLPTLARSFLICLQIMSEARFOXYLEG 173  
 Db 117 ERWAHQSRQQTPLGLQALTHGIS---FPRSGGNDEEKKARTLIVITVQAEARFRYTSN 173

Qy 174 EMRTTR 180  
 Db 174 RVVRSIQ 180

RESULT 11  
 RIPI\_LUFCY STANDARD; PRT; 250 AA.  
 ID RIPI\_LUFCY  
 AC P222651;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-AUG-1991 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Ribosome-inactivating protein luffin-B (rRNA N-glycosidase)  
 DE (EC 3.2.2.22).  
 OS Luffa cylindrica (Smooth gourd) (Sponge gourd)  
 OC Buxaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; Rosidae;  
 OC eurosids I; Cucurbitales; Cucurbitaceae; Luffa.  
 OX NCBI\_TaxId=3670;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RN Yamada T., Ohki S.T., Osaki T.;  
 RN "Cloning and analysis of a CDNA coding a putative ribosome-  
 inactivating protein from *Cucumis ficifolii*";  
 RT inactivating protein from *Cucumis ficifolii*.  
 RL Plant Biotechnol. 17:337-340(2000).  
 CC -!- CATALYTIC ACTIVITY: Endonucleolysis of the N-glycosidic bond at one  
 specific adenine on the 28S rRNA.  
 CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 CC -!- TYPE 1 RIP SUBFAMILY.

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 or send an email to license@isb-sib.ch).

CC DR EMBL: AB045560; BAB19677.1; -.  
 CC DR HSSP: P16094; 1AHC.  
 CC DR InterPro; IPR001574; RIP.  
 CC DR Pfam; PF00161; RIP; 1.  
 CC DR PRINTS; PR00336; SHIGARICIN.  
 CC DR PROSITE; PS00275; SHIGA\_RICIN.  
 CC DR Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;  
 CC KW Toxin; Signal; SIGNAL; 1 21 POTENTIAL.  
 CC FT CHAIN 22 286 PUTATIVE RIBOSOME-INACTIVATING PROTEIN.  
 CC FT ACT SITE 185 185 BY SIMILARITY.  
 CC DR HSSP: P16094; 1AHC.  
 CC DR InterPro; IPR001574; RIP.  
 CC DR "Complete amino acid sequence of luffin-b, a ribosome-inactivating  
 protein from sponge gourd (*Luffa cylindrica*) seeds.";  
 CC RL Agric. Biol. Chem. 55:229-238(1991).  
 CC -!- CATALYTIC ACTIVITY: Endonucleolysis of the N-glycosidic bond at one  
 specific adenine on the 28S rRNA.  
 CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 CC -!- TYPE 1 RIP SUBFAMILY.

DR PIR; JN0108; JN0108.  
 DR HSSP: P16094; 1AHC.  
 DR InterPro; IPR001574; RIP.  
 DR PRINTS; PR00336; SHIGARICIN.  
 DR PROSITE; PS00275; SHIGA\_RICIN; 1.  
 DR Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;  
 KW Toxin. ACT SITE 160 160 BY SIMILARITY.  
 SQ SEQUENCE 250 AA; 27293 MW; F01ADC8A1078700 CRC64;

Query Match 9 INFITAGATVQSYTNFIRAVRGRLTNRYGL---VGLPI-----NQFILVELSNHAELSTV 58  
 Best Local Similarity 33.2%; Score 290; DB 1; Length 250;  
 Matches 61; Conservative 48; Mismatches 57; Indels 18; Gaps 4;

Qy 9 INFITAGATVQSYTNFIRAVRGRLTNRYGL---VGLPI-----NQFILVELSNHAELSTV 58  
 Db 3 VFSLSGDSKSKYSKFKITLRCALPSKCKVSNIPLLPSASSGASRYTLMQNSYDAKAIT 62

Qy 59 IALDVNTAYVGYRAGNSAYFFHPDNQEDAAITHLFPTDVQNRFTFAFGCGNYDRLQLAG 118  
 Db 63 MADVTNVYIMGYLNNTSYF---ANESDAKASQYVFKGSTLVTIPSGNVRLOQAAG 119

Qy 119 NLRENTIELGNGPFLPEAISALAYYYSTGGTQLPTLARSFLICLQIMSEARFOXYLEGEMRTR 178  
 Db 120 KRCRKPQGFLRDAATSIFYDSD---TAAAAAFVILQTTAEASRFKTFEGQIITER 174

Qy 179 IRYN 182  
 Db 175 IPKN 178

RESULT 13

RIPA\_LJFECY STANDARD; PRT; 277 AA.  
 ID RIPA\_LJFECY  
 AC P81446; (Rel. 37, Created)  
 DT 15-DEC-1992 (Rel. 37, Last sequence update)  
 DT 01-DEC-1992 (Rel. 24, Last annotation update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Ribosome-inactivating protein luffin-alpha precursor (rRNA N-glycosidase) (EC 3.2.2.22).  
 DE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Strptophyta; Embryophyta; Tracheophyta; Santalales; Santalaceae; Viscum. [1]  
 OC NCBI\_TaxID=3972;  
 OC RN 3670;  
 OC RN 1;  
 RN SEQUENCE FROM N.A.  
 RC TISSUE=seed;  
 RX MEDLINE=92288316; PubMed=16001156;  
 RA Matzuka J., Habuka N., Miyano M.; Masuta C., Koiwai A.;  
 RA Nucleotide sequence of cDNA encoding alpha-luffin, a ribosome-  
 RT inactivating protein from Luffa cylindrica.";  
 RL Plant Mol. Biol. 18:1199-1202(1992).  
 CC -!- CATALYTIC ACTIVITY: Endohydrolisis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.  
 CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 CC -!- TYPE 1 RIP SUBFAMILY.  
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 CC EMBL; X23471; CAA429.1; -.  
 DR PTR: S22494; S22494.  
 DR HSSP; PI6094; 1AHC.  
 DR InterPro; IPR01574; RIP.  
 DR Pfam; PF00161; RIP; 1.  
 DR PRINTS; PRO0396; SHIGARICIN.  
 DR PROSITE; PS00275; SHIGA\_RICIN; 1.  
 KW Plant defense; Hydrolase; Toxin; Lectin.  
 KW Antiviral; Protein synthesis inhibitor; Hydrolyase; Toxin; Signal.  
 FT SIGNAL 1 19 RIBOSOME-INACTIVATING PROTEIN LUFFIN-  
 FT CHAIN 20 277 ALPHA.  
 FT ACT SITE 179 BY SIMILARITY.  
 SQ SEQUENCE 277 AA; 30212 MW; EAL7FC2798C25AC CRC64;  
 Query Match 9 INFITAGATVQSYNTNTRAVGRGLTRVGLIN-----ORFLIVELSNHAELSV 57  
 Matches 62; Best Local Similarity 33.3%; Fred. No. 1.2e-18; Length 277;  
 Mismatches 42; N mismatches 62; Indels 20; Gaps 4;  
 Qy 81 TIAADTVNAYVGYRAGNSAFFFPHQEDAEITHLTQVNYTAAFSRKYRQGQIE 137  
 Db 22 VRFSLSGSSSTSYSKFIGDLKALPSN-GTYNTTILLSSASGASRYTMILSNYDGKAI 80  
 Qy 58 TIALDVTNAYVGYRAGNSAFFFPHQEDAEITHLTQVNYTAAFSRKYRQGQIE 117  
 Db 138 GKIREKPLGFALDSAITLHYD5----NESDAKLASQVFRGSTTIVLPYSNEYLKQTAA 192  
 Qy 178 RIRYNR 183  
 Db 193 RISKNQ 198  
 Qy 118 GNLRNIELNGPLEEALAYYYSTGGTQPLTLARSFLICQIMSEAAFRQYIGEMRT 177  
 Db 139 TAGAVVQSTTNFIRAVR----GRLTNRVGL----PNN-QRFLIVELSNHAELSVL 59  
 Qy 60 ALDVTNAYVGYRAGNSAFFFPHQDNQEDAEITHLTQVNYTAAFSRKYRQGQIE 119  
 Db 69 AIDVTNAYVAYQGDQSFLR-DAPRGA--THLFTGT-TRSSLPLFNGSPDLYRAGH 124

RESULT 14  
 MLA\_VISAL ID - MLA\_VISAL

AC P81446; (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-DEC-1998 (Rel. 41, Last annotation update)  
 DE Beta-galactoside specific lectin I A chain (MLA) (ML-I A) (rRNA N-glycosidase) (EC 3.2.2.22).  
 OS Viscum album (European mistletoe).  
 OC Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Santalales; Santalaceae; Viscum. [1]  
 OC NCBI\_TaxID=3972;  
 RN RP SEQUENCE.  
 RC STRAIN=Subsp. album;  
 RX MEDLINE=97134581; PubMed=8980141;  
 RA Soler M.H., Stoeva S., Schwamborn C., Wilhelm S., Stiefel T., Voelter W.;  
 RA "Complete amino acid sequence of the A chain of mistletoe lectin I.";  
 RL FEBS Lett. 399:153-157(1996).  
 CC -!- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S rRNA. THE B CHAIN BINDS TO CELL RECEPTORS AND PROBABLY FACILITATES THE ENTRY INTO THE CELL OF THE A CHAIN; B CHAINS ARE ALSO RESPONSIBLE FOR CELL AGGLUTINATION (LECTIN ACTIVITY).  
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.  
 CC -!- SUBUNIT: Disulfide-linked dimer of A and B chains.  
 CC -!- PHARMACEUTICAL: due to its immunomodulatory effects it is being studied in clinical trials in cancer patients as it may slow the growth of cancer cells and be an effective treatment for solid tumors.  
 CC -!- MISCELLANEOUS: TWO ISOFORMS OF MLA EXIST: GLYCOSYLATED FORM MLA, AND NON-GLYCOSYLATED FORM MLA'.  
 CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 CC -!- TYPE 2 RIP SUBFAMILY.  
 DR PIR: P00018; PD0018.  
 DR HSSP; P11140; 1AHC.  
 DR InterPro; IPR01574; RIP.  
 DR Pfam; PF00161; RIP; 1.  
 DR PRINTS; PRO0396; SHIGARICIN.  
 DR PROSITE; PS00275; SHIGA\_RICIN; FALSE NEG.  
 DR Plant defense; Hydrolase; Toxin; Repeat; Glycoprotein; Lectin.  
 FT ACT SITE 165 BY SIMILARITY.  
 FT CARBOHYD 165 BY SIMILARITY.  
 FT CARBOHYD 112 112 N-LINKED (GLCNAC. . . ).  
 FT VARIANT 15 15 BY SIMILARITY.  
 FT VARIANT 66 66 BY SIMILARITY.  
 FT VARIANT 112 112 N -> T (IN MLA').  
 FT VARIANT 116 116 P -> T (IN MLA').  
 FT VARIANT 133 134 DQ -> E (IN MLA').  
 FT VARIANT 140 140 T -> S (IN MLA').  
 FT VARIANT 144 144 F -> Y (IN MLA').  
 FT VARIANT 151 151 T -> A (IN MLA').  
 FT VARIANT 179 179 Y -> D (IN MLA').  
 FT VARIANT 184 184 A -> E (IN MLA').  
 FT VARIANT 190 190 V -> M (IN MLA').  
 FT VARIANT 223 223 PP -> ST (IN MLA').  
 FT VARIANT 231 231 T -> S (IN MLA').  
 FT VARIANT 235 235 D -> S (IN MLA').  
 SQ SEQUENCE 254 AA; 28478 MW;

Query Match 13 TAGAVVQSTTNFIRAVR----GRLTNRVGL----PNN-QRFLIVELSNHAELSVL 59  
 Best Local Similarity 31.8%; Pred. No. 2.3e-18; Gaps 10;  
 Matches 79; Conservative 30; Mismatches 53; Indels 47;

Qy 9 THQTGEYEFRTTILRDYSSGSFSNEIPLRQSTIPVSDAQRFLVLTNOGSDSYTA 68

120 LRENIELNGPLEEAIASLYYYSTGGTQLPTLARSFIIOMISEAARF-----QYI 171  
 QY :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
 Db -RDPDPLGIDOLIQSVTALRF--PGGSTRTRARSILILIQMSEAAENPILWRYQYI 180  
 QY 172 E-----GEMTRIRYN 182  
 :|:|:|:  
 Db 181 NSGASFLPDVYMLETSWGQOSTVOHS 209

RESULT 15

RPI1_MONCH	STANDARD;	PRT;	286 AA.
ID RPI1_MONCH			
AC P24697;			
DT 01-APR-1990 (Rel. 14, Created)			
DT 01-MAR-1992 (Rel. 21, Last sequence update)			
DE Ribosome-inactivating protein monordin I precursor [rRNA N-glycosidase] (EC 3.2.2.22) (Alpha-monomcharin) (Alpha-MMC).			
DE Monordica charantia (Bitter gourd) (Balsam pear).			
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytina; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eudicots I; Cucurbitales; Cucurbitaceae; Momordica.			
OX [1]			
RN TAXID=3673;			
RP SEQUENCE FROM N.A.			
RC TISSUE=seed;			
RX MEDLINE=91159486; PubMed=20014044;			
RA Ho W.K.-K., Liu S.C., Shaw P.-C., Yeung H.W., Ng T.B., Chan W.Y.,			
RA "Cloning of the cDNA of alpha-monomcharin: a ribosome inactivating protein." Protein. Biochim. Biophys. Acta 1088:311-314 (1991).			
RN [2]			
RP SEQUENCE OF 24-38.			
RC TISSUE=Seed;			
RX MEDLINE=9326691; PubMed=2753596;			
RA Montecuccchi P.C., Lazzarini A.M., Barbieri L., Stirpe F., Soria M., Lappi D.;			
RA "N-terminal sequence of some ribosome-inactivating proteins."			
RT "N-terminal sequence of some ribosome-inactivating proteins." Int. J. Pept. Protein Res. 33:263-267 (1999).			
RN [3]			
RP SEQUENCE OF 24-70.			
RC TISSUE=Seed;			
RX MEDLINE=9005108; PubMed=3262509;			
RA Casellas P., Dussossoy D., Falasca A.T., Barbieri L., Cenini P., Stirpe F.; Guillermot J.C., Ferrara P., Bolognesi A., Trichokirin, a ribosome-inactivating protein from the seeds of Trichosanthus kirilowii, purification, partial characterization and use for preparation of immunotoxins." Eur. J. Biochem. 176:581-588 (1988).			
RN [4]			
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).			
RX MEDLINE=94356447; PubMed=8075985;			
RA Ren J., Wang Y., Dong Y., Stuart D.I.; RT "Crystal structure of monordin, a type I ribosome-inactivating protein from the seeds of Momordica charantia." FEBS Lett. 342:154-158 (1994).			
RN [5]			
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).			
RX MEDLINE=95144383; PubMed=7619010;			
RA Hussain J., Tickle I.J., Wood S.P.; RT "Studies on crystal structures, active-centre geometry and depurinating mechanism of two ribosome-inactivating proteins." Eur. J. Biochem. 309:285-298 (1995).			
CC :- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenine on the 28S rRNA.			

-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 TYPE 1 RIP SUBFAMILY.

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CC EMBL: X57682; CAR40869\_1; -. DR DIR; S14273; RLPGCG.

CC DR PDB; IAHA; 22-JUN-94. DR PDB; IAHB; 22-JUN-94.

CC DR PDB; IAHC; 22-JUN-94. DR PDB; IMOM; 31-MAY-94.

CC DR PDB; IMRG; 07-FEB-95. DR PDB; IMRH; 07-FEB-95.

CC DR PDB; IMRI; 07-FEB-95. DR PDB; IFRQ; 21-NOV-01.

CC GlycoSuiteDB; P16094; -. DR InterPro; IPR01574; RIP.

CC PRINTS; PR00396; SHIGARICIN. DR PROSITE; PS00275; SHIGA\_RICIN; 1.

CC KW Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin; Signal; Glycoprotein; 3D-structure.

CC KW SIGNAL 1 23 RIBOSOME-INACTIVATING PROTEIN MONORDIN I.

CC FT CHAIN 24 269 MISSING IN MATURE PROTEIN.

CC FT PROPEP 270 286 CARBOHYD 183 250 N-LINKED (GLCNAC. . .).

CC FT STRAND 25 28 /FTID=CAR\_000082.

CC FT HELIX 34 47

CC FT STRAND 50 54

CC FT TURN 55 56

CC FT STRAND 57 60

CC FT HELIX 66 69

CC FT STRAND 70 76

CC FT TURN 78 79

CC FT STRAND 82 88

CC FT TURN 89 92

CC FT STRAND 93 99

CC FT TURN 100 101

CC FT STRAND 102 105

CC FT HELIX 109 114

CC FT TURN 115 117

CC FT TURN 120 121

CC FT STRAND 124 127

CC FT HELIX 134 141

CC FT HELIX 145 147

CC FT STRAND 150 150

CC FT HELIX 152 162

CC FT TURN 163 163

CC FT HELIX 167 186

CC FT STRAND 187 187

CC FT HELIX 188 195

CC FT STRAND 240 241

CC FT TURN 246 250

CC FT STRAND 251 252

CC FT HELIX 254 258

CC FT TURN 259 259

CC FT STRAND 260 260

CC FT HELIX 263 263

CC SEQUENCE 266 268 SQ 31532 MN; E1B013ABEBC216CF CRC64;

Query Match      28.4%;    Score 270.5;    DB 1;    Length 286;  
 Best Local Similarity      35.4%;    Pred. No. 4;    1e-10;  
 Matches      64;    Conservative      40;    Mismatches      58;    Indels      19;    Gaps      5;

Qy	9 INFITAGATVQSYTNFIRAVRGLTNR--VGILPI-----NQRFLIVELSNHAELSVI 58
Db	25 VSFRLSGADPRTSIGMFIDRNALPFRKVNINPLIPSVSGARYLMLHJENYDGKTIT 84
Qy	59 LALDVTNAVVGYRAGNSAYFFHDNQDAEATHLEPTDVQNYTPAFGGNDREQLA 117
Db	85 VADVINVNTIMGLADTSYF--NEPAEELSQYVPRDARKITLPYSGNYERLOIAA 141
Qy	118 GNLRNTELGNGPLEEAISALYYSTGGTOLPLARSPLICOMISEARFOYIEGEMRT 177
Db	142 GKPREKIPIGLPALESAITLHYDS---TAAGALLVLIQTTAEARFKIEQQQE 196
Qy	178 R 178
Db	197 R 197

Search completed: February 10, 2004, 16:23:25  
 Job time : 6.17124 secs

Result No.	Score	Query Match	Length	DB ID	Description	SUMMARIES
1	934.5	98.3	541	10 Q41174	Q41174 ricinus com	
2	370	38.9	580	10 Q94BW3	Q94bw3 cinnamomum	
3	370	38.9	580	10 Q94BW4	Q94bw4 cinnamomum	
4	366	38.5	581	10 Q94BW5	Q94bw5 cinnamomum	
5	364	38.3	549	10 Q9FV22	Q9Fv22 cinnamomum	
6	335.5	35.3	289	10 Q94KE4	Q94ke4 cinnamomum	
7	333.5	35.1	289	10 Q41216	Q41216 trichosanth	
8	327.5	34.4	247	10 Q9LRE3	Q9lre3 trichosanth	
9	326	34.3	563	10 Q04367	Q04367 sambucus ni	
10	323	34.0	564	10 Q9AVR2	Q9avr2 sambucus eb	
11	313.5	33.0	270	10 Q8LPV7	Q8lpv7 trichosanth	
12	310.5	32.6	270	10 Q41611	Q41611 trichosanth	
13	310	32.6	252	10 Q38760	Q38760 abrus preca	
14	308	32.4	528	10 Q06076	Q06076 abrus preca	
15	306	32.2	563	10 Q94SS2	Q94ss2 sambucus ni	
16	306	32.2	563	10 Q8GT32	Q8gt32 sambucus ni	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	934.5	98.3	541	10 Q41174	Q41174 ricinus com
2	370	38.9	580	10 Q94BW3	Q94bw3 cinnamomum
3	370	38.9	580	10 Q94BW4	Q94bw4 cinnamomum
4	366	38.5	581	10 Q94BW5	Q94bw5 cinnamomum
5	364	38.3	549	10 Q9FV22	Q9Fv22 cinnamomum
6	335.5	35.3	289	10 Q94KE4	Q94ke4 cinnamomum
7	333.5	35.1	289	10 Q41216	Q41216 trichosanth
8	327.5	34.4	247	10 Q9LRE3	Q9lre3 trichosanth
9	326	34.3	563	10 Q04367	Q04367 sambucus ni
10	323	34.0	564	10 Q9AVR2	Q9avr2 sambucus eb
11	313.5	33.0	270	10 Q8LPV7	Q8lpv7 trichosanth
12	310.5	32.6	270	10 Q41611	Q41611 trichosanth
13	310	32.6	252	10 Q38760	Q38760 abrus preca
14	308	32.4	528	10 Q06076	Q06076 abrus preca
15	306	32.2	563	10 Q94SS2	Q94ss2 sambucus ni
16	306	32.2	563	10 Q8GT32	Q8gt32 sambucus ni

\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RP SEQUENCE FROM N.A. MEDLINE=92338377; PubMed=16333311;

RX Robert L.M. Tregeair J.W. Lord J.M.; RT "Molecular cloning of ricin";

RL Targeted Diagn. Ther. 7:81-97 (1992).

CC SPECIFIC ADENOSINE ON THE 28S RNA.

CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.

CC EMBL: S40366; AAB2582.1; -.

DR HSSP; P02879; 1BR6.

DR InterPro; IPR000772; Ricin\_B\_lectin.

DR InterPro; IPR001574; RIP.

DR InterPro; IPR001440; Somatotropin.

DR Pfam; PF00652; Ricin\_B\_lectin; 6.

DR Pfam; PF00161; RIP; 1.

DR PRINTS; PR03936; SHIGARICIN.

DR SMART; SM00454; RICIN.

DR PROSITE; PS05031; RICIN\_B\_LECTIN; 2.

DR PROSITE; PS00275; SHIGA\_RICIN; 1.

DR PROSITE; PS00338; SOMATOTROPIN\_2; 1.

KW Hydrolase; Toxin.

PT NON\_TER 1

SEQUENCE 541 AA; 60281 MW; 2B7B2CDEF1F2E9D9 CRC64;

SQ

Query	Match 98.3%; Score 934.5; DB 10; Length 541;	Qy	173 GEMRTRI 179
Best Local Similarity 93.4%; Pred: No. 1.8e-80;	Mismatches 0; Indels 13; Gaps 1;	Db	208 YRVRESI 214
Matches 185; Conservative 0;			
Db			
Qy	1 IFKQYPIINFATGATVSYNTNFIRAVGRLT-----NRVGLPINOREFTL 47		
Db	1 IFKQYPIINFATGATVSYNTNFIRAVGRLT-----NRVGLPINOREFTL 60		
Qy	48 ELSNHAESVTALDVNTAYVGYTRAGNSAYFFPDNQDAEAITHFTDQNRYTFAFG 107	RESULT 3	
Db	61 ELSNHAESVTALDVNTAYVGYTRAGNSAYFFPDNQDAEAITHFTDQNRYTFAFG 120	Q94BWA	PRELIMINARY:
Qy	108 GNYDLRQLAGNRENIELGGNPLBEAISALYYSTGGTQLPTLARSFICOMISEAR 167	AC Q94BWA	PRT: 580 AA.
Db	121 GNYDLRQLAGNRENIELGGNPLBEAISALYYSTGGTQLPTLARSFICOMISEAR 180	DT 01-DEC-2001 (TREMBLrel. 19, Created)	
Qy	168 FOYIEGMRTRIYRNRS 185	DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)	
Db	181 FOYIEGMRTRIYRNRS 198	DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)	
Qy	SEQUENCE FROM N.A.	DE Type 2 ribosome-inactivating protein cinnamomin II precursor (EC 3.2.2.22) (rRNA N-glycosidase).	
Db	RP Yang Q., Gong Z.Z., Liu W.Y.;	OS Cinnamomum camphora (Camphor tree).	
Qy	RT Molecular cloning of three type 2 RIP (ribosome-inactivating protein genes encoding cinnamomin proteins and study of their expression patterns);	CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE POSITION.	
Db	RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.	CC -!- SPECIFIC ADENOSINE ON THE 28S RNA.	
Qy	RT Submitted (JUN-2001) (TREMBLrel. 19, Last sequence update)	CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.	
Db	RT Submitted (JUN-2003) (TREMBLrel. 23, Last annotation update)	DR EMBL; AY039802; AAK82459.1; -	
Qy	DE (EC 3.2.2.22) (rRNA N-glycosidase).	DR InterPro; IPR000772; Ricin_B_lectin.	
Db	OS Cinnamomum camphora (Camphor tree).	DR InterPro; IPR01574; RIP_B_fam; IPR0652; Ricin_B_lectin; 6.	
Qy	OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; OC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.	DR Pfam; PF00161; RIP; I_lectin; 6.	
Db	OX NCBI_TaxID=13429;	DR PRINTS; PR0396; SHIGARICIN.	
Qy	RN SEQUENCE FROM N.A.	DR SMART; SM00456; RICIN; 2.	
Db	RA Yang Q., Gong Z.Z., Liu W.Y.;	DR PROSITE; PS50231; Ricin_B_LECTIN; 2.	
Qy	RT Molecular cloning of three type 2 RIP (ribosome-inactivating protein genes encoding cinnamomin proteins and study of their expression patterns);	FT SIGNAL 1 32 POTENTIAL.	
Db	RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.	FT CHAIN 33 580 TYPE 2 RIBOSOME-INACTIVATING PROTEIN CINNAMOMIN II.	
Qy	CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE POSITION.	FT SIGNAL 28 580 AA; 64265 MW; 37E4289ECCB0CBPF CRC64;	
Db	CC -!- SPECIFIC ADENOSINE ON THE 28S RNA.	FT SIGNAL 28; Mismatches 52; Indels 18; Gaps 6;	
Qy	DR EMBL; AY039803; AAK2460.1; -	Query Match 38.9%; Score 370; DB 10; Length 580;	
Db	DR InterPro; IPR000772; Ricin_B_lectin.	Best Local Similarity 47.6%; Pred. No. 1.2e-26;	
Qy	DR Pfam; PF00652; Ricin_B_lectin; 6.	DR PROSITE; PS50231; Ricin_B_LECTIN; 2.	
Db	DR SMART; SM00456; SHIGARICIN.	DR PRINTS; PR0396; SHIGARICIN.	
Qy	DR SIGNAL 1 32 POTENTIAL.	DR SMART; SM00456; SHIGARICIN.	
Db	FT SIGNAL 33 580 CINNAMOMIN III.	DR PROSITE; PS50231; Ricin_B_LECTIN; 2.	
Qy	SQ SEQUENCE 580 AA; 64421 MW; 940DFOE7FB558 CRC64;	DR PRINTS; PR0396; SHIGARICIN.	
Db	6 YPLINPITAGATVSYNTNFIRAVGRLTN-----RVLGINQRSLVLSN-H 52	DR SMART; SM00456; SHIGARICIN.	
Qy	33 YQTVTFITKNAKTSYQFIEALRAQLAQSYRAGNSAYFFHPDNQDAEAITHFTDQNRYTFAFGNDR 92	DR SIGNAL 1 32 POTENTIAL.	
Db	53 AELSVTFLADVTNAYVGYTRAGNSAYFFHPDNQDAEAITHFTDQNRYTFAFGNDR 112	FT SIGNAL 1 32 POTENTIAL.	
Qy	53 AELSVTFLADVTNAYVGYTRAGNSAYFFHPDNQDAEAITHFTDQNRYTFAFGNDR 112	FT SIGNAL 1 32 POTENTIAL.	
Db	93 ADFPVTLADVTNAYVAYRTGSQFFREDNPD-PATENLLPDIK-RYPFPSSSYTD 149	FT SIGNAL 1 32 POTENTIAL.	
Qy	113 LEOLAGNIRENIELGGNPLEEAISALYYSTGGTQLPTLARSFICOMISEARFOYIE 172	FT SIGNAL 1 32 POTENTIAL.	
Db	150 LERVGGERRETILGMDPLENATISALWISNL-NOQRALARSLIVVVAEVRFIE 207	FT SIGNAL 1 32 POTENTIAL.	
Qy	RESULT 4	DB 150 LERVGGERRETILGMDPLENATISALWISNL-NOQRALARSLIVVVAEVRFIE 207	
Db	Q94BMS	Q94BMS PRELIMINARY; PRT: 581 AA.	
Qy	AC Q94BMS	AC Q94BMS	
Db	DT 01-DEC-2001 (TREMBLrel. 19, Created)	DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)	
Qy	DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)	DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)	
Db	DE Type 2 ribosome-inactivating protein cinnamomin I precursor (EC 3.2.2.22) (rRNA N-glycosidase).	DE Type 2 ribosome-inactivating protein cinnamomin I precursor (EC 3.2.2.22) (rRNA N-glycosidase).	

DR	InterPro; IPR000772; Ricin_B_lectin.
DR	InterPro; IPR001574; RIP.
DR	Pfam; PF000652; Ricin_B_lectin; 5.
DR	Pfam; PF00161; RIP; 1.
DR	PRINTS; PR0396; SHIGARICIN.
DR	SMART; SM00458; RICIN.
DR	PROSITE; PS0232; RICIN_B_LECTIN; 2.
KW	Hydrolase; Toxin.
FT	NON_TER 1 1 MW 02607FE607CA4A0 CRC64;
SQ	SEQUENCE 549 AA; 60648 MW; 02607FE607CA4A0 CRC64;
Query Match	38.3%; Score 364; DB 10; Length 549;
Best Local Similarity	47.6%; Pred. No. 4.2e-26;
Matches	89; Conservative 25; Mismatches 55; Indels 18; Gaps 5;
Qy	6 YPLINTFTAGATVQSTNTPIAVRGLTN-----RVLGEINQRFLVLSN-H 52
Db	1 YQRTVFTTKAKPTSQFIEFLRAQLASGEEPHGIYVMDRSTYDSSKCFILVEWSNVA 60
Qy	53 AELSVTIALDVNTAYGYRAGNSAYFFHPDNQEDAFAITHLFTDQNRVTFAGGGNYDR 112
Db	61 ADSEVTIALDVNTAYVAYRTQSFFLREDNPD-PATENILPDTK-RYTFPFSSEYTD 117
Qy	113 LEQLGNIRENLIGQPLEEALAYYYSTGGTQPLTLPASRFLIQMISEAARPOXIE 172
Db	118 LESVAGGEREEILLGMDPLENATSAWLISNL--NOQRALARSLIVVQTMYAEAVRFRFIE 175
Qy	173 GEHRTRI 179
Db	176 YRVFGSI 182
RESULT 6	
Q94KE4	Q94KE4 PRELIMINARY; PRT; 289 AA.
ID	Q94KE4; DT 01-DEC-2001 (TREMBLrel. 19, Created)
AC	Q94KE4; DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
CC	01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE	Trichosanthin precursor (EC 3.2.2.22) (rrna N-glycosidase).
GN	TCS
OS	Trichosanthos kirilowii (Mongolian snake gourd).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
EC	eurosid I; Cucurbitales; Cucurbitaceae; Trichosanthes.
OX	NCBI_TaxID=3677;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Yuan H., Wang L., Wang Y., An, C., Chen Z.;
RL	Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC	-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RRNA.
CC	-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR	EMBL; AF562323; AKS2930.1; -.
DR	InterPro; IPR01574; RIP.
DR	Pfam; PF00161; RIP; 1.
DR	PRINTS; PR0396; SHIGARICIN.
DR	PROSITE; PS00275; SHIGA_RICIN; 1.
KW	Hydrolase; Sigma; Toxin.
FT	SIGNAL 1 23 POTENTIAL.
FT	CHAIN 24 31706 MW; TRICHOSANTHIN.
SQ	SEQUENCE 289 AA; 31706 MW; A6D5602549CA5657 CRC64;
Query Match	35.3%; Score 335.5; DB 10; Length 289;
Best Local Similarity	39.0%; Pred. No. 9.1e-24;
Matches	71; Conservative 42; Mismatches 50; Indels 19; Gaps 4;
Qy	9 INFITAGATVQSTNTPIAVRGLTN-----RVLGEINQRFLVLSN-HAELSVT 58
Db	25 VSFRSLGATSSYGVFSNLRKAPNERYDIPLLRSLLPGSQRAYLHLTNYADETIS 84
Qy	59 LALDDTNAVGYRAGNSAYFFHDNQEAA-LATHL 117

Db		85 VAIDVNVYIMGYRAGDTSYFF --NEASATEARYVFDSMRKLTPLPSGNYELQLQTA 141					
Qy	118 GNLRENIELGNGPLEAISALYYSTGGTOLPLTARSFLICIQMISEARFOYEGEMRT 177						
Db	142 GKIRENIEPLGLDALSATLTFYNNAN----SASAALVLIQSTSEARYKFTEQQIGK 196						
Qy	178 RI 179						
Db	197 RV 198						
	RESULT 7						
	Q41216_ PRELIMINARY;	PRT;	289 AA.				
	ID Q41216;						
	AC Q41216;						
	DT 01-NOV-1996 (TREMBLrel. 01; Created)						
	DT 01-NOV-1996 (TREMBLrel. 01; Last sequence update)						
	DT 01-OCT-2002 (TREMBLrel. 22; Last annotation update)						
	DE Trichosanthin (EC 3.2.2.22) (rRNA N-glycosidase).						
	GN TRICHOSANTHIN, TCS.						
	OS Trichosanthes kirilowii (Mongolian snake-gourd).						
	OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eucommias; Cucurbitales; Cucurbitaceae; Trichosanthes.						
	OC NCBI_TAXID=3677;						
	RN [1] SEQUENCE FROM N.A.						
	SEQUENCE_ID=94271613; PubMed=8003348;						
	RX HSSP; P09989; IMRJ.						
	RA Zheng H.; Wang B.; Shaw P.; Yeung H.;						
	RT "[Cloning and DNA sequencing of the gene encoding trichosanthin]."						
	RL I Chuan Hsueh Pao 21:42-51 (1994).						
	CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 2BS RNA.						
	CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.						
	DR EMBL: S70176; AAB31048; 1. -.						
	DR HSSP; P09989; IMRJ.						
	DR InterPro; IPR001574; RIP.						
	DR Pfam; PF001661; RIP; 1.						
	DR PRINTS; PR00396; SHIGARICIN.						
	DR PROSITE; PS00275; SHIGA_RICIN; 1.						
	KW Hydrolase; Toxin.						
	SQ SEQUENCE 289 AA; 3160 MW; 286AC14DA8BCA175 CRC64;						
	Query Match 35.1%; Score 333.5; DB 10; Length 289;						
	Best Local Similarity 39.0%; Pred. No. 1.4e-23;						
	Matches 71; Conservative 42; Mismatches 50; Indels 19; Gaps 4						
	Qy 9 INFITGATVQSYINFEIRAYGRILIN-----RVCLPINQRFILVELNSNAELSVT 58						
	Db 25 VSFRLSGATSSYYGTFSINLRKALPNERKLVDIPLLRSSSLPSQRVALHTNYADTIS 84						
	Qy 59 LALDDVTNAATVGYRAGNSAYEFPHDNQEDA-BAITHLFTDVQNRYPFAGGNYDRLEQLA 117						
	Db 85 VAIIDTVTSMVGYRAGDTSYFF--NEASATEARYVFDSMRKLTPLPSGNYELQLQTA 141						
	Qy 118 GNLRENIELGNGPLEAISALYYSTGGTOLPLTARSFLICIQMISEARFOYEGEMRT 177						
	Db 142 GKIRENIEPLGLDALSATLTFYNNAN----SASAALVLIQSTSEARYKFTEQQIGK 196						
	Qy 178 RI 179						
	Db 197 RV 198						
	RESULT 8						
	Q9IRE3_ PRELIMINARY;	PRT;	247 AA.				
	ID Q9IRE3;						
	AC Q9IRE3;						
	DT 01-OCT-2000 (TREMBLrel. 15; Created)						
	DT 01-OCT-2000 (TREMBLrel. 15; Last sequence update)						
	DT 01-OCT-2002 (TREMBLrel. 22; Last annotation update)						
	DE Trichobakin (EC 3.2.2.22) (rRNA N-glycosidase) (Fragment).						
	GN TBK.						

Trichosanthes sp. Bac Kan 8-98.  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes  
 NCBI\_TaxID=118182;

[1] SEQUENCE FROM N.A.  
 Phan Van Chi, Nguyen Thuy Ha, Le Tran Binh;  
 "Genomic DNA Clone for mature typ-1 ribosome-inactivating protein from  
 Trichosanthes sp. sample 01 Bac Kan 8-98 Vien CNSH (Hanoi).";  
 Submitted (FEB-2000) to the EMBL/GenBank/DBJ database;  
 -|- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
 SPECIFIC ADENOSINE ON THE 28S RNA.  
 -|- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 EMBL: AB039324; BA92530.1; -.  
 HSSP; P09989; 1MRU.  
 InterPro: IPR01574; RIP.  
 Pfam: PF00161; RIP; 1.  
 PRINTS; PR00396; SHIGARICIN.  
 PROSITE; PS00275; SHIGA\_RICIN; 1.  
 Hydrolase; Toxin.

NON_TER	1	247	247	AA:	27199	MW:	89811AC32892FF03F	CRC64;
SEQUENCE								

Query Match Score 34.4%; Score 37.5%; DB 10; Length 247;  
 Best Local Similarity 39.0%; Pred. No. 4.2e-23; Gaps 4;  
 Matches 71; Conservative 42; Mismatches 50; Indels 19;

9 INFPTGATVOSYNTNFTRAVRGRLTN-----RVGLP1NQRFLVELSNHAELSVT 58  
 2 VSFRSGATSSSYGVITNSLRKALPPKRYDIPPLASTLPCSQVALIHLTNAYETIS 61

59 LALDTINATVYGYRAGNSAYFHPDQEDA-EAITHLFTDVQNRTFAFGGNYDRLEQLA 117  
 60 :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
 62 VAIDVTNVNTMVGYRAGDTSYF---MEASATAAKVYKDFDAKRTVLPYSGNVYERLOQIA 118

118 GNLTENTIELNGPLEAISALYYSSGGTOLPTLARSFIICOMISPAARFQYIGEMRT 177  
 119 GKIRENPIGLPALDSAITILFYNNAN----SAASALMVLIQSTSAAARYKFIEQQIGK 173

178 RI 179  
 :  
 174 RV 175

SILT 9  
 4367 PRELIMINARY; PRT; 563 AA.  
 004367  
 004367;  
 01-JUL-1997 (REMBLrel. 04, Created)  
 01-JUL-1997 (REMBLrel. 04, Last sequence update)  
 01-OCT-2002 (REMBLrel. 22, Last annotation update)  
 Ribosome inactivating protein precursor (EC 3.2.2.22) (tRNA  
 N-Glycosidase);  
 Sambucus nigra (European elder).  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Asteridae; campanulids; Dipsacales; Asteraceae; Sambucus.  
 NCBI\_TaxID=4202;

[1] SEQUENCE FROM N.A.  
 MEDLINE=981120232; PubMed=9450339;  
 Van Damme B.J., Roy S., Barre A., Rouge P., Van Leuven F.,  
 Peumans W.J.;  
 "The major elderberry (Sambucus nigra) fruit protein is a lectin  
 derived from a truncated type 2 ribosome-inactivating protein.";  
 Plant J. 12:1251-1260 (1997).  
 -|- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
 SPECIFIC ADENOSINE ON THE 28S RNA.  
 -|- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 EMBL: U76524; AAC15886.1; -.  
 HSSP; P02879; 2AA1.





卷之三

AVL.	Sambucus nigra (European elder). Eukaryota; Viridiplantae; Streptophyta; Embryophytina; Magnoliophyta; eudicotyledons; Asteridae; campanulids; Dipsacales; Adoxaceae; N-glycosidase).	PRT;	563 AA.
Q945S2	PRELIMINARY;	PRT;	
Q945S2;			
Q945S2;	(TREMBI)re1. 19, Created)		
01-DEC-2001	(TREMBI)re1. 19, Last sequence upd		
01-DEC-2001	(TREMBI)re1. 23, Last annotation u		
01-MAR-2003	(TREMBI)re1. 23, Last annotation u		
	Ribosome-inactivating protein (BC 3.2.2.22) (		
	N-glycosidase).		
NCBI_TaxID=4202;			
[1]	SEQUENCE FROM N.A.		
TISSUE=Leaf;			
Van Damme E.J.M.;			
"Characterization and cloning of lectins and			
proteins from Sambucus nigra leaves.";			
Submitted (AUG-2001) to the EMBL/GenBank/DBJ			
-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE			
SPECIFIC ADENOSINE ON THE 2'8S RNA.			
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACT			
EMBL; AF049135; AAL04123.1; -!			
InterPro; IPR007261; Ricin_B_lectin.			
InterPro; IPR001374; RIP.			
Pfam; PF001621; Ricin_B_lectin; 6.			
Pfam; PF001621; RIP; 1.			

GenCore version 5.1.6  
 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2004, 16:13:20 ; Search time 34.0993 Seconds  
 (without alignments)  
 930.966 Million cell updates/sec

Title: US-10-083-336A-10  
 Perfect score: 1029

Scoring table: BLOSUM62  
 Sequence: MIFPKQYPLINFTTAGATVQ.....RFQYIEGMRTRIVNRRSA 200

Scoring table: Gapext 0.5

Searched: 1107863 seqs, 158725573 residues

Total number of hits satisfying Chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%  
 Listing first 45 summaries

Database : A\_Genesed\_19Jun03,\*

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  2: /SIDSI/gcadata/geneseq/geneseqp-emb1/AA1981.DAT:*
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  8: /SIDSI/gcadata/geneseq/geneseqp-emb1/AA1987.DAT:*
  9: /SIDSI/gcadata/geneseq/geneseqp-emb1/AA1988.DAT:*
  10: /SIDSI/gcadata/geneseq/geneseqp-emb1/AA1989.DAT:*
  11: /SIDSI/gcadata/geneseq/geneseqp-emb1/AA1990.DAT:*
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  21: /SIDSI/gcadata/geneseq/geneseqp-emb1/AA2000.DAT:*
  22: /SIDSI/gcadata/geneseq/geneseqp-emb1/AA2001.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	1024	99.5	267 14 AR37290	Ricin A chain. Un
2	1024	99.5	267 16 AR63902	Ricin A-chain (RTA
3	1024	99.5	290 18 AW25136	Ricin A-chain ribo
4	1024	99.5	290 18 AW21699	Ricin A-chain R.P.
5	1024	99.5	332 8 AAP70097	Ricin A. Escheric
6	1024	99.5	332 8 AAP70838	Sequence of Ricinu
7	1024	99.5	332 10 AAP95639	Ricin A encoded by
8	1024	99.5	554 16 AAP70827	Anti-Dataramt immu
9	1024	99.5	562 10 AAP90079	Ricin D. Ricinus

Title: US-10-083-336A-10	Perfect score: 1024	Search time 34.0993 Seconds	930.966 Million cell updates/sec	Modified castor bean sequence of Ricinu
Scoring table: BLOSUM62	Sequence: MIFPKQYPLINFTTAGATVQ.....RFQYIEGMRTRIVNRRSA 200	Gapext 0.5	99.5	Castorbean ricin.
Scoring table: Gapext 0.5	Sequence: MIFPKQYPLINFTTAGATVQ.....RFQYIEGMRTRIVNRRSA 200	99.5	Castor bean ricin.	
Scoring table: Gapext 0.5	Sequence: MIFPKQYPLINFTTAGATVQ.....RFQYIEGMRTRIVNRRSA 200	99.5	Ricinus communis r	
Scoring table: Gapext 0.5	Sequence: MIFPKQYPLINFTTAGATVQ.....RFQYIEGMRTRIVNRRSA 200	99.5	Castor bean prepro	
Scoring table: Gapext 0.5	Sequence: MIFPKQYPLINFTTAGATVQ.....RFQYIEGMRTRIVNRRSA 200	99.5	Castor bean prepro	
Scoring table: Gapext 0.5	Sequence: MIFPKQYPLINFTTAGATVQ.....RFQYIEGMRTRIVNRRSA 200	99.5	Sequence of ricin-	
Scoring table: Gapext 0.5	Sequence: MIFPKQYPLINFTTAGATVQ.....RFQYIEGMRTRIVNRRSA 200	99.5	Sequence of prepro	
Scoring table: Gapext 0.5	Sequence: MIFPKQYPLINFTTAGATVQ.....RFQYIEGMRTRIVNRRSA 200	99.5	Castor bean prepro	
Scoring table: Gapext 0.5	Sequence: MIFPKQYPLINFTTAGATVQ.....RFQYIEGMRTRIVNRRSA 200	99.5	Sequence of G-FIT.	
Scoring table: Gapext 0.5	Sequence: MIFPKQYPLINFTTAGATVQ.....RFQYIEGMRTRIVNRRSA 200	99.5	Sequence of Ricinu	
Scoring table: Gapext 0.5	Sequence: MIFPKQYPLINFTTAGATVQ.....RFQYIEGMRTRIVNRRSA 200	99.5	Biosynthetic multi	
Scoring table: Gapext 0.5	Sequence: MIFPKQYPLINFTTAGATVQ.....RFQYIEGMRTRIVNRRSA 200	99.5	Preproricin.	
Scoring table: Gapext 0.5	Sequence: MIFPKQYPLINFTTAGATVQ.....RFQYIEGMRTRIVNRRSA 200	99.5	Ricin A. Synthetic	
Scoring table: Gapext 0.5	Sequence: MIFPKQYPLINFTTAGATVQ.....RFQYIEGMRTRIVNRRSA 200	99.5	DNA sequence of ri	
Scoring table: Gapext 0.5	Sequence: MIFPKQYPLINFTTAGATVQ.....RFQYIEGMRTRIVNRRSA 200	99.5	Ricin A from PICII	
Scoring table: Gapext 0.5	Sequence: MIFPKQYPLINFTTAGATVQ.....RFQYIEGMRTRIVNRRSA 200	99.5	Amino acid sequenc	
Scoring table: Gapext 0.5	Sequence: MIFPKQYPLINFTTAGATVQ.....RFQYIEGMRTRIVNRRSA 200	99.5	Ricin A gene produ	
Scoring table: Gapext 0.5	Sequence: MIFPKQYPLINFTTAGATVQ.....RFQYIEGMRTRIVNRRSA 200	99.5	Ricin A chain (RTA	
Scoring table: Gapext 0.5	Sequence: MIFPKQYPLINFTTAGATVQ.....RFQYIEGMRTRIVNRRSA 200	99.5	Ricin A. Synthetic	
Scoring table: Gapext 0.5	Sequence: MIFPKQYPLINFTTAGATVQ.....RFQYIEGMRTRIVNRRSA 200	99.5	Castor oil plant a	
Scoring table: Gapext 0.5	Sequence: MIFPKQYPLINFTTAGATVQ.....RFQYIEGMRTRIVNRRSA 200	99.5	R. communis agglut	
Scoring table: Gapext 0.5	Sequence: MIFPKQYPLINFTTAGATVQ.....RFQYIEGMRTRIVNRRSA 200	99.5	Mature alpha-trich	
Scoring table: Gapext 0.5	Sequence: MIFPKQYPLINFTTAGATVQ.....RFQYIEGMRTRIVNRRSA 200	99.5	Trichosanthin (a r	
Scoring table: Gapext 0.5	Sequence: MIFPKQYPLINFTTAGATVQ.....RFQYIEGMRTRIVNRRSA 200	99.5	Trichosanthin. Tr	
Scoring table: Gapext 0.5	Sequence: MIFPKQYPLINFTTAGATVQ.....RFQYIEGMRTRIVNRRSA 200	99.5	Trichosanthin from	
Scoring table: Gapext 0.5	Sequence: MIFPKQYPLINFTTAGATVQ.....RFQYIEGMRTRIVNRRSA 200	99.5	Trichosanthin from	
Scoring table: Gapext 0.5	Sequence: MIFPKQYPLINFTTAGATVQ.....RFQYIEGMRTRIVNRRSA 200	99.5	Trichosanthin prot	
Scoring table: Gapext 0.5	Sequence: MIFPKQYPLINFTTAGATVQ.....RFQYIEGMRTRIVNRRSA 200	99.5	Encodes Chinese cu	
Scoring table: Gapext 0.5	Sequence: MIFPKQYPLINFTTAGATVQ.....RFQYIEGMRTRIVNRRSA 200	99.5	Alpha-trichosanthin	
Scoring table: Gapext 0.5	Sequence: MIFPKQYPLINFTTAGATVQ.....RFQYIEGMRTRIVNRRSA 200	99.5	Chinese cucumber a	

#### ALIGNMENTS

RESULT 1  
 ID AAR37290 standard; protein; 267 AA.

AC AAR37290;

XX



XX Hey TD, Morgan AER, Walsh TA;  
 PI XX WPI; 1997-352934/33.  
 XX DNA encoding pro-ribosome inactivating proteins - inactive  
 PT precursors of ribosome inactivating proteins; can be expressed in  
 PT eukaryotic cells without causing cell death  
 XX Claim 4; Column 91-94; 186pp; English.  
 XX AAW2136 represents a Ricin A-chain ribosome inhibitory protein (RIP)  
 CC which was engineered to contain a selectively removable internal Peptide  
 CC linker sequence separating the alpha and beta units of the RIP. When  
 CC separated the two units regain activity and are capable of inactivating  
 CC eukaryotic ribosomes and hence preventing protein production. Many  
 CC different RIPs may be produced with an internal linker including  
 CC maize RIP, Trichosanthin, Ricin A-chain, Abrin-A A-chain and  
 CC Saporin. The RIPs can be used in the construction of therapeutic  
 CC toxins targeted to specific cells such as tumour cells via the  
 CC attachment of a targeting polypeptide, e.g. monoclonal antibody.  
 CC A further use is in HIV therapy (see US469303). There is interest  
 CC in expressing RIP recombinantly in host eukaryotic cells, because of  
 CC the capacity to provide correct post-translational processing. However,  
 CC RIPs effectively inhibit protein synthesis in eukaryotic cells resulting  
 CC in cell death. Since the inactive RIP proteins are not cytotoxic to  
 CC eukaryotic cells, they can be recombinantly expressed in such cells and  
 CC then converted to active RIP proteins.  
 CC (Updated on 25-MAR-2003 to correct PF field.)  
 XX Sequence 290 AA;

Query Match 99.5%; Score 1024; DB 18; Length 290;  
 Best Local Similarity 100.0%; Pred. No. 8.4e-101;  
 Matches 199; Conservative 0; Mismatches 0; Gaps 0;

Qy 2 IFPKQYPIINFTAGATVQSYTNFIAVRGLRTGADVRHEIPIVLPNVLQPNQRFLV 61  
 Db 25 IFPKQYPIINFTAGATVQSYTNFIAVRGLRTGADVRHEIPIVLPNVLQPNQRFLV 84  
 Qy 62 ELSNHAEELSTVLLALDVTNTAVGTRAGNSAYFFPDNQEDAETHLFTDVQNYTFARG 121  
 Db 85 ELSNHAEELSTVLLALDVTNTAVGTRAGNSAYFFPDNQEDAETHLFTDVQNYTFARG 144

Qy 122 GNYDLEQLAGNLRENTIELNGPLFEAISALYYSTGGTQLPTLARSFLICOMISEAR 181  
 Db 145 GNYDLEQLAGNLRENTIELNGPLFEAISALYYSTGGTQLPTLARSFLICOMISEAR 204

Qy 182 FQYIGEMRTRIYNRSA 200  
 Db 205 FQYIGEMRTRIYNRSA 223

RESULT<sup>4</sup>  
 AAW21699  
 ID AAW21699 standard; Protein; 290 AA.  
 AC AAW21699;  
 XX DT 25-MAR-2003 (updated)  
 DT 26-SEP-1997 (first entry)  
 XX OS Ricin communis.  
 DE Ricin A-chain RIP.

XX Pro-Ribosome Inactivating Protein; prorIP; peptide linker; cancer;  
 KW inactivation; eukaryotic ribosome; alpha fragment; beta fragment;  
 KW inhibitor; Protein Synthesis; N-glycosidase; glycosidic bond; liver;  
 KW rat; ribosomal 28S RNA; cellular proliferation; HIV-infected T cell.  
 XX Location/Qualifiers  
 XX Key  
 FT Region 152..162

/note= "Position of possible insertion of internal peptide linker sequence"

FT PT XX US5635384-A.  
 PN XX 03-JUN-1997.  
 PD XX 26-JAN-1995; 95US-0378761.  
 PR 09-DEC-1992; 92US-0987927.  
 PR 11-JUN-1990; 90US-0355636.  
 PR 26-JAN-1995; 95US-0378761.  
 PA (DOWC ) DOWBLANCO.  
 PA Hey TD, Morgan AER, Walsh TA;  
 PA Hey TD, Morgan AER, Walsh TA;  
 PA 1997-309831/28.  
 PA Inactive precursor of maize ribosome-inactivating protein - also  
 PT chimeric ribosome inactivating protein precursors containing  
 PT internal linker sequences  
 PA Column 91-94; 121PP; English.  
 PA PT PT PT PT  
 PA PS Column 91-94; 121PP; English.  
 PA PS Claim 2:  
 PA PS The sequences given in AAW21698-710 represent Ribosome Inactivating  
 CC Proteins (RIP's), which may be used in the construction of the  
 CC proIP of the invention. The proIP has a selectively removable,  
 CC internal Peptide Linker. The precursor sequence is incapable of  
 CC inactivating eukaryotic ribosomes, but can be converted by removal  
 CC of the linker into protein having alpha and beta fragments and being  
 CC capable of inactivating eukaryotic ribosomes. RIPs are potent  
 CC inhibitors of eukaryotic protein synthesis. They possess a highly  
 CC specific N-glycosidase activity which cleaves the Glycosidic bond of  
 CC adenine 434 of rat liver ribosomal 28S RNA. RIP's selectively inhibit  
 CC cellular proliferation of cells e.g. cancer cells and HIV-infected T  
 CC cells. The inactive proRIP proteins make it possible to provide protein  
 CC synthesis inhibitors with uses in practical and improved ways not before  
 CC possible. The RIP can be used to make cytotoxic conjugates.  
 CC (Updated on 25-MAR-2003 to correct PF field.)  
 SQ Sequence 290 AA;

Query Match 99.5%; Score 1024; DB 18; Length 290;  
 Best Local Similarity 100.0%; Pred. No. 8.4e-101;  
 Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IFPKQYPIINFTAGATVQSYTNFIAVRGLRTGADVRHEIPIVLPNVLQPNQRFLV 61  
 Db 25 IFPKQYPIINFTAGATVQSYTNFIAVRGLRTGADVRHEIPIVLPNVLQPNQRFLV 84  
 Qy 62 ELSNHAEELSTVLLALDVTNTAVGTRAGNSAYFFPDNQEDAETHLFTDVQNYTFARG 121  
 Db 85 ELSNHAEELSTVLLALDVTNTAVGTRAGNSAYFFPDNQEDAETHLFTDVQNYTFARG 144

Qy 122 GNYDLEQLAGNLRENTIELNGPLFEAISALYYSTGGTQLPTLARSFLICOMISEAR 181  
 Db 145 GNYDLEQLAGNLRENTIELNGPLFEAISALYYSTGGTQLPTLARSFLICOMISEAR 204

Qy 182 FQYIGEMRTRIYNRSA 200  
 Db 205 FQYIGEMRTRIYNRSA 223

RESULT<sup>5</sup>  
 AAW21699  
 ID AAW21699 standard; protein; 332 AA.  
 AC AAP70097  
 XX DT 09-APR-1991 (First entry)  
 XX AC AAP70097;  
 DE Ricin A.

RESULT 5  
 AAP70097  
 ID AAP70097 standard; protein; 332 AA.  
 XX AC AAP70097;  
 DE AAP70097;

			/note="A-chain" 315...332
			/note="B-chain"
PT	Region		
FT			
FT			
FT			
XX			
PN	EP237676-A.		
XX			
PD	23-SEP-1987.		
XX			
PP	13-NOV-1986;	86EP-0308877.	
XX			
PR	07-MAR-1986;	86US-0837583.	
XX			
PA	( CETU ) CETUS CORP.		
PA	( CHIR ) CHIRON CORP.		
XX			
PI	Piatak M;		
XX			
DR	WPI; 1987-265177/38.		
DR	N-PSDB; AAN70519.		
XX			
PT	New non-glycosylated ricin precursor by recombinant DNA procedures will be obtained.		
PT	purified and soluble prods.		
PT			
XX			
PS	Disclosure; Fig 1; 112pp; English		
XX			
CC	The full-length sequences encoded in the library were obtained using messenger RNA from rat liver.		
CC	CC (AAN70525), putative ricin B (AAN70526),		
CC	CC then probing the library to reveal the location of the putative ricin B gene.		
CC	CC Library was probed using the 35-S labeled cRNA probe.		
CC	CC AAN70520, AAN70521, AAN70522) were obtained.		
CC	CC plasmids containing cDNA inserts obtained from the library.		
CC	CC Sequences encoding ricin B using the 35-S labeled cRNA probe.		
CC	CC Insertions can be placed into expression vectors for mutagenesis.		
CC	CC The mutagenesis may be used to place the insertion site at the beginning of the message.		
CC	CC Insertions can be placed into expression vectors for mutagenesis.		
CC	CC Insertions can be placed into expression vectors for mutagenesis.		
CC	CC Insertions can be placed into expression vectors for mutagenesis.		
CC	CC Insertions can be placed into expression vectors for mutagenesis.		
CC	CC Insertions can be placed into expression vectors for mutagenesis.		
CC	CC Insertions can be placed into expression vectors for mutagenesis.		
XX			
SQ	Sequence 332 AA;		
Qy	Query Match 99.5%;	Score 7	
	Best Local Similarity 100.0%;		
	Matches 199;	Conservative 0;	
Qy	2 IPKQKPYINFTAGATVQSYTH		
Db	36 IPKQKPYINFTAGATVQSYTH		
Qy	62 ELSNHAELSVTLADVTNAYVY		
Db	96 ELSNHAELSVTLADVTNAYVY		
Qy	122 GNYDRLEQLAGNLRENIELGNG		
Db	156 GNYDRLEQLAGNLRENIELGNG		
Qy	182 FQYIEGENMTRTRINRNSA 20		
Db	216 FQYIEGENMTRTRINRNSA 23		
RESULT	7		
ID	AAP95639		
ID	AAP95639 standard; protein; 332		
XX			
AC	AAP95639;		
XX			
DT	25-MAR-2003 (updated)		
DT	31-OCT-2002 (updated)		

DT	13-AUG-1990	(first entry)	QY	182 FQYIEGEMTRIYNRSA 200
XX	DE	Ricin A encoded by insert from plasmid PRA123.	Db	216 FQYIEGEMTRIYNRSA 234
XX	KW	Plasmid PRA123; ricin-A; ricin-B; cytotoxicity.		
XX	OS	Ricinus communis.		
OS	Synthetic.			
XX	XX		RESULT 8	
	Key	Location/Qualifiers	ID AAR70827	
FT	Peptide	1..35 /label= leader sequence	AC AAR70827;	
FT	Peptide	36..302 /label=A-chain	XX	
FT	Peptide	303..314 /label=linker	DT 25-MAR-2003 (updated)	
FT	Peptide	315..332 /label=B-chain	DT 31-AUG-1995 (first entry)	
XX	PN	EP335476-A.	XX	
XX	PD	04-OCT-1989.	DB	
XX	XX	89BP-1989;	XX	
.PF	19-JAN-1989;	89BP-0201162.	Key	1..27
XX	XX		Peptide	/label= Sig_Peptide
PR	08-FEB-1984;	84US-0578115.	FT	/note= "phoA signal sequence"
PR	08-FEB-1984;	84US-0578121.	FT	28..145
PR	09-FEB-1984;	84US-0578122.	FT	/label= HEAVY
PR	07-SEP-1984;	84US-0648759.	FT	/note= "MAB 4197X heavy chain"
PR	20-SEP-1984;	84US-0653515.	FT	148..166
XX	PA	(CETU ) CETUS CORPORATION.	FT	/label= LINER
XX	PA	Gelfand D, Lawyer FC, Horn G, Greenfield L, Nitecki D, Kaplan D;	FT	Domain
PI	PIatak MJ;		FT	/note= "MAB 419X light chain"
XX	DR	WPI; 1989-286959/40.	FT	Domain
DR	N-PSDB; AA991281.		FT	/label= RICIN-A
XX	PT	recombinant vectors expressing ricin chains or diphtheria toxin -used for prodn. of new immunotoxin conjugates with monoclonal antibodies, having high cell specificity and good extracellular stability.	FT	Peptide
XX	PS	Disclosure: Fig 14; 54pp; English.	FT	549..554
XX	PS		FT	/label= TAG
CC	CC	Plasmid RA123 (ATCC No. 39799) carries the entire coding sequence for ricin A, as well as codons for 12 As joining the A to the B chain.	FT	/note= "hexa-histidine tail"
CC	CC	Following modification for ease of manipulation the plasmid was used to construct expression vectors which express the conjugates in host cells.	XX	
CC	CC	(Updated on 31-OCT-2002 to add missing OS field.)	PI	Gould RM, Kelleher PJ, Wallace TL, Wood MS;
CC	CC	(Updated on 25-MAR-2003 to correct PF field.)	XX	WPI; 1995-082036/11.
CC	CC	(Updated on 25-MAR-2003 to correct PR field.)	DR	N-PSDB; AA985386.
XX	XX	(Updated on 25-MAR-2003 to correct PI field.)	XX	New single chain immuno:toxin - binds specifically to epithelial cells, for inhibiting development of sec. cataracts after extra:capsular cataract extraction.
XX	XX	Sequence 332 AA;	PT	
Query Match	99.5%	Score 1024; DB 10; Length 332;	XX	
Best Local Similarity	100.0%	Pred. No. 1..100; Mismatches 0; Indels 0; Gaps 0;	PS	
Matches	199; Conservative		PS	
QY	2	IFPKQYPINFTAGATYQSYTNFIRAVRGRLLTGADRVHETPVLPRVGIPINQRFLIV 61	CC	The immunotoxin given in AAR70827 comprises the heavy and light chain variable regions of anti-lens epithelial IgG3 MAb 4197X linked to ricin-A and a hexa-histidine tag. The DNA construct encoding the immunotoxin was expressed from phB19 in E. coli.
Db	36	IFPKQYPINFTAGATYQSYTNFIRAVRGRLLTGADRVHETPVLPRVGIPINQRFLIV 95	CC	(Updated on 25-MAR-2003 to correct PN field.)
QY	62	ELSNHAEISVTLALDVNTNAYVGYRAGNSAYFFPHDNOEADAEATHLFTDVONYRTPAFG 121	CC	
Db	96	ELSNHAEISVTLALDVNTNAYVGYRAGNSAYFFPHDNOEADAEATHLFTDVONYRTPAFG 155	CC	
QY	122	GNYDRLEQLAGLNRLRENTIELNGNPLEEAISALYYXYSTGTQLPLARSPTICQMISEAR 181	Sequence	554 AA;
Db	156	GNYDRLEQLAGLNRLRENTIELNGNPLEEAISALYYXYSTGTQLPLARSPTICQMISEAR 215	Query Match	99.5%; Score 1024; DB 16; Length 554;
			Best Local Similarity	100.0%; Pred. No. 2..100; Mismatches 0; Indels 0; Gaps 0;
			Matches	199; Conservative

Db	96	ELSNHAEALSTVTLADYNTAYVGYRANSAYFFHDQEDAEITHLPTDVQNRYTFAKG	155
QY	1122	GNYDRLEQLAGLNRLRENTLGNGPLEEISALYYSTGGTQLPLARSFLICOMISEAR	181
Db	156	GNYDRLEQLAGLNRLRENTLGNGPLEEISALYYSTGGTQLPLARSFLICOMISEAR	215
QY	182	FQYIEGEMRTRIYNRSA	200
Db	216	FQYIEGEMRTRIYNRSA	234
<b>RESULT 10</b>			
	AAG78104	standard; Protein; 565 AA.	
ID	AAG78104		
XX			
AC	AAG78104;		
XX	DT	27-NOV-2001	(first entry)
XX	DE	Modified castor bean prororicin	(SEQ ID 10).
XX	KW	Castor bean plant; prororicin; A chain; B chain;	
KW	human immunodeficiency virus infection; HIV; toxin; antiviral agent;		
KW	retroviral infection; anti-HIV; viricide; viral protease.		
XX	OS	Ricinus communis	
XX	Chimeric - Human immunodeficiency virus type 2.		
PH	Key	Location/Qualifiers	
FT	Peptide	1..24	
FT		/label= Signal_peptide	
FT	Protein	25..565	
FT		/label= Prororicin	consists of the ricin A chain, a linker
FT		peptide, and the ricin B chain. Prororicin is	proteolytically cleaved between the A chain and
FT		the linker to yield mature ricin."	
Protein		25..291	
FT		/label= Ricin A chain	
FT		/note= "N-Glycosidase"	
FT	Peptide	292..303	
FT		/label= Linker_Peptide	
FT	Cleavage-site	296..297	
FT		/label= HIV_protease_cleavage_site	
Protein		304..565	
FT		/label= Ricin B chain	
FT		/note= "Galactose/N-acetylgalactosamine-binding lectin"	
XX	PN	WO20010393-A1.	
XX	PD	23-AUG-2001.	
XX	PF	15-FEB-2001; 2001WO-US05282.	
XX	PR	16-FEB-2000; 2000US-0162759.	
XX	PA	(BECH-) BECHTEL BIWXT IDAHO LLC.	
XX	PI	Keefer WK, Ward TE;	
XX	XX		
DR	WPI; 2001-581908/65.		
DR	N-PSDB; AAI6445.		
XX	XX	Novel composition comprising toxin e.g., ricin based antiviral compound	
PT	PT	useful for treating viral infections such as human immunodeficiency	
PT	PT	virus infection.	
PS	PS	Example 1; Page 59-63; 66pp; English.	
XX	XX	The sequence relates to the amino acid sequence of a modified prororicin	
CC	CC	protein encoded by WO010393-A1. The invention relates to a novel toxin	
CC	CC	(e.g. ricin) based antiviral agent which is toxic to virus-infected	

cells, but non-toxic to uninfected cells. The invention has anti-HIV and virocidic activities. The agent is able to enter all HIV susceptible cells, and not just cells known to act as host cells for the virus. The antiviral agent remains inert in a cell unless the cell is infected with the HIV virus, where the viral protease activates it. Richin's mechanism of action is through inactivation of cellular ribosomes and enhancement of binding of the antiviral agent to Galactose residues on cell surfaces, and its cellular internalisation. The invention is useful for treating human immunodeficiency virus infection and other viral infections, especially retroviral infections. The antiviral agent is activated in viral particles or early-stage infected cells, killing the cells upon infection and effectively preventing the integration of the viral genome into the host genome thereby preventing the latency/rebound problem.

FT	Peptide	303..314	Db	216 FQYIEGENRTRIRYNRSA 234
FT	Domain	315..576		
FT		/1label= B-domain		
XX				
PN	US5668255-A.			
XX				
PD	16-SEP-1997.			
XX				
PF	04-AUG-1993;	93US-0102387.		
XX				
PR	27-JUN-1991;	91US-0722484.		
PR	07-JUN-1984;	84US-0618199.		
PR	25-APR-1985;	85US-0722808.		
PR	07-JUN-1985;	85US-0745554.		
PR	22-DEC-1989;	89US-0456095.		
PR	14-JUN-1990;	90US-0532276.		
PR	04-AUG-1993;	93US-0102387.		
XX				
PA	(SERA-) SERAGEN INC.			
XX				
PI	Murphy JR;			
XX				
WPI;	1997-470103/43.			
DR	N-PSDB; AAT91638.			
XX				
PT	New hybrid molecules for delivery of agents to cells - comprise a binding domain of a cell binding ligand and a portion of a translocation domain of a protein			
PT				
XX				
PS	Example 4; Fig 11A-B; 30pp; English.			
XX				
This polypeptide comprises the castorbean cytotoxin, ricin DNA (see AAT91638) encoding the enzymatic A domain and a portion of the A-to-B linker peptide of ricin was used to construct a ricin-diphtheria toxin B'-interleukin-2 gene that was expressed in E. coli. The hybrid protein can be isolated and used to treat conditions involving over-production of cells bearing IL2 receptors, such as certain T-cell lymphomas and organ transplant rejection crises. The hybrid inactivates ribosomes in cells bearing IL2 receptors, resulting in cessation of protein synthesis and death of target cells. Claimed hybrid proteins comprise a translocation domain and a cell binding domain from e.g. a hormone, growth factor or polypeptide toxin. The hybrid molecules can be used for the delivery of agents (e.g. therapeutic genes, detectable labels) into cells. The use of a translocation mechanism ensures that the hybrid will be effective in relatively low doses, since a high proportion of the substance of interest will be taken into the targeted cells. The hybrid molecules can be manufactured as a single hybrid recombinant protein, permitting reproducibility, consistency, and the precise control of composition.				
CC	(Updated on 25-MAR-2003 to correct PF field.)			
XX				
SQ	Sequence 576 AA;			
Qy	Query Match Score 1024; DB 18; Length 576;			
Best Local Similarity 99.5%; Pred. No. 2.1e-100;				
Matches 199: Conservative 0; Mismatches 0; Indels 0;				
Db	2 LFPKQPIINFTTAGTVQSTNFIRAVRGLTGADRVHEIPVLPNVLGPINORFILY 61			
	36 LFPKQPIINFTTAGTVQSTNFIRAVRGLTGADRVHEIPVLPNVLGPINORFILY 95			
Qy	62 ELSNHABLSVTLADYVNAVGYRAGNSAFFHPNQEDEATHLFTDVQNRTFAFG 121			
Db	96 ELSNHABLSVTLADYVNAVGYRAGNSAFFHPNQEDEATHLFTDVQNRTFAFG 155			
Qy	122 GMYDRLEQLAGNLRENIELGNGPLERAIAYYYSTGGTQPTLARSFLICIQMISEAAR 181			
Db	156 GMYDRLEQLAGNLRENIELGNGPLERAIAYYYSTGGTQPTLARSFLICIQMISEAAR 215			
Qy	182 FQYIEGENRTRIRYNRSA 200			

Query Match Score 1024; DB 20; Length 576;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-100;  
 Mismatches 0; Indels 0; Gaps 0;  
 Matches 199; Conservative 0; Gaps 0;

Qy	2 IPKQYPIINFTAGATQSYTNFIRAVRGLTTGADVRHEIPVLPNRVGLPINORFLV 61
Db	36 IPKQYPIINFTAGATQSYTNFIRAVRGLTTGADVRHEIPVLPNRVGLPINORFLV 95
Qy	62 ELSNHAEISVTLALDVNTAAYVGYRAGNSAYFHPNQEDAITHLFTDQNRTFAFG 121
Db	96 ELSNHAEISVTLALDVNTAAYVGYRAGNSAYFHPNQEDAITHLFTDQNRTFAFG 155
Qy	122 GNYDRLEQLAGNLRENTIELGNQPLEFAISALYYSTGGTQLPTLARSFLICIQMISEAR 181
Db	156 GNYDRLEQLAGNLRENTIELGNQPLEFAISALYYSTGGTQLPTLARSFLICIQMISEAR 215
Qy	182 FQYIEGEMRTRIYNRSA 200
Db	216 FQYIEGEMRTRIYNRSA 234

## RESULT 14

AAV78592 standard; Protein; 576 AA.  
 XX AAV78592;  
 AC AAV78592;  
 XX DT 05-MAY-2000 (first entry)  
 XX DE Ricinus communis ricin protein sequence.  
 XX  
 Ricin toxin; hybrid protein; translocation domain; cell destruction;  
 KW cell binding domain; generic deficiency disease; cell targeting; cancer;  
 KW adipocyte; enzyme delivery; anti-viral; HIV.  
 XX  
 Ricinus communis.  
 OS OS6022950-A.  
 PN XX  
 PD 08-FEB-2000.  
 XX  
 PF 07-JUN-1995; 95US-0479510.

XX  
 PR 07-JUN-1994; 84US-0618199.  
 PR 27-JUN-1991; 91US-0722484.  
 PR 25-APR-1985; 85US-0726808.  
 PR 07-JUN-1985; 85US-0742554.  
 PR 22-DEC-1989; 89US-0456095.  
 PR 14-JUN-1990; 90US-0538276.  
 PR 04-AUG-1993; 93US-0102387.  
 XX  
 PA (SERA-) SERAGEN INC.  
 XX Murphy JR;  
 XX  
 DR WPI; 2000-160390/14.  
 DR N-PSDB; AAZ30019.

XX  
 PT New two-part hybrid protein comprising a translocation domain and a cell-binding domain, for treating genetic deficiency diseases, cancer and HIV infections -  
 XX  
 PS Example 4: Fig 11; 32pp; English.

XX This sequence represents the Ricinus communis ricin protein sequence. The toxin can be included in the hybrid protein of the invention and used to destroy or modify the cell that the hybrid protein is targeted to. The hybrid protein comprises a first part which is a portion of the binding domain of a cell-binding ligand, effective to cause the hybrid molecule to bind to a cell of an animal. The second part comprises a portion of a translocation domain of a naturally occurring protein (e.g. the translocation domain of diphtheria toxin) the second part translocates the third part across the cytoplasmic membrane and into the cytosol of

the cell. The third part comprises a chemical entity to be introduced into the cell, where each of the first and third part is non-native with respect to naturally occurring protein, and the covalent bond attaching the second and third part is cleavable. The toxin represented by the present sequence can form part of the third portion of the hybrid protein. The cell binding domain binds to a specific cell and the translocation domain transfers the hybrid molecule across the cell membrane into the cytosol. The third part of the protein, linked to the translocation domain through a cleavable bond, can then carry out its function. The hybrid molecules are useful for treating genetic deficiency diseases by delivering to affected cells an enzyme supplying the missing function, to supplement cellular levels of a particular enzyme or a scarce precursor or cofactor, to direct toxins or other poisons to destroy particular cells (such as adipocytes, cancer cells, or virus-infected cells), and to counter viral infections such as HIV by introducing into appropriate cells antibodies to viral proteins.

Sequence 576 AA;  
 Query Match 99.5%; Score 1024; DB 21; Length 576;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-100;  
 Mismatches 0; Indels 0; Gaps 0;  
 Matches 199; Conservative 0; Gaps 0;

Qy	2 IFPKQYPIINFTAGATQSYTNFIRAVRGLTTGADVRHEIPVLPNRVGLPINORFLV 61
Db	36 IFPKQYPIINFTAGATQSYTNFIRAVRGLTTGADVRHEIPVLPNRVGLPINORFLV 95
Qy	62 ELSNHAEISVTLALDVNTAAYVGYRAGNSAYFHPNQEDAITHLFTDQNRTFAFG 121
Db	96 ELSNHAEISVTLALDVNTAAYVGYRAGNSAYFHPNQEDAITHLFTDQNRTFAFG 155
Qy	122 GNYDRLEQLAGNLRENTIELGNQPLEFAISALYYSTGGTQLPTLARSFLICIQMISEAR 181
Db	156 GNYDRLEQLAGNLRENTIELGNQPLEFAISALYYSTGGTQLPTLARSFLICIQMISEAR 215
Qy	182 FQYIEGEMRTRIYNRSA 200
Db	216 FQYIEGEMRTRIYNRSA 234

RESULT 15  
 AAG78301 standard; Protein; 576 AA.  
 ID AAG78301;  
 XX  
 AC AAG78301;  
 XX DT 15-NOV-2001 (first entry)  
 XX DE Castor bean preproricin protein (SEQ ID 2).  
 XX DE Castor bean plant; preproricin; ricin; A chain; B chain;  
 KW human immunodeficiency virus infection; HIV; toxin; antiviral agent;  
 KW retroviral infection; anti-HIV; virucide activity; viral protease.  
 XX  
 OS Ricinus communis.  
 PH Key Location/Qualifiers  
 FT Peptide 1..35  
 FT /label= Signal peptide  
 FT Protein 36..302  
 FT /label= Ricin A chain  
 FT /note= "N-glycosidase"  
 FT Peptide 303..314  
 FT /label= Linker peptide  
 FT /note= "Cleaved during activation of ricin"  
 FT Protein 315..576  
 FT /label= Ricin B chain  
 FT /note= "Galactose/N-acetylgalactosamine-binding lectin"  
 XX WO200160393-A1.  
 XX  
 PD 23-AUG-2001.

PF 15-FEB-2001; 2001WO-US05282.  
 XX PR 16-FEB-2000; 2000US-0182759.

XX PA (BECH-) BECHTEL BWXT IDAHO LLC.  
 XX PI Keener WK, Ward TE;

XX DR WPI; 2001-581908/65.  
 DR N-PSDB; AA164138.

XX PT Novel composition comprising toxin e.g., ricin based antiviral compound  
 PT useful for treating viral infections such as human immunodeficiency  
 virus infection.

XX Disclosure: Page 50-54; 66pp; English.

XX The sequence relates to preproricin protein encoded by the DNA sequence  
 CC given in AAI64138. The invention relates to a novel toxin (e.g., ricin)  
 CC based antiviral agent which is toxic to virus-infected cells, but  
 CC non-toxic to uninfected cells. The invention has anti-HIV and virucide  
 CC activities. Its mechanism of action is through inactivation of cellular  
 CC ribosomes and enhancement of binding of the antiviral agent to galactose  
 CC residues on cell surfaces, and its cellular internalisation. The  
 CC invention is useful for treating human immunodeficiency virus infection  
 CC and other viral infections, especially retroviral infections. The  
 CC antiviral agent is activated in viral particles or early-stage infected  
 CC cells, killing the cells upon infection and effectively preventing the  
 CC integration of the viral genome into the host genome thereby preventing  
 CC the latency/rebound problem. The agent enters all HIV susceptible cells,  
 CC and not just cells known to act as host cells for the virus. The  
 CC antiviral agent remains inert in a cell until degraded in it, unless the  
 CC cell is infected with the virus, where the viral protease activates it.

XX Sequence 576 AA;

Query Match 99.5%; Score 1024; DB 22; Length 576;

Best Local Similarity 100.0%; Pred. No. 2.1e-100;  
 Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	2	I FPKOYPLINFTTAGVOSTXNFTRAVGRGLTCGADVRHEIPVLPNRYGLPQNQRFLIV	61
Db	36	I FPKOYPLINFTTAGVOSTXNFTRAVGRGLTCGADVRHEIPVLPNRYGLPQNQRFLIV	95
Qy	62	E LSHAEELSTLALQUTNATVYTGAGNSAYFHDNQEAETHLFTDVQRYTEAFG	121
Db	96	E LSHAEELSTLALQUTNATVYTGAGNSAYFHDNQEAETHLFTDVQRYTEAFG	155
Qy	122	GNYDRLQLQNLRENIELGNGPLEBAISALLYSTGGTOLPTLARSFLICOMISEAR	181
Db	156	GNYDRLQLQNLRENIELGNGPLEBAISALLYSTGGTOLPTLARSFLICOMISEAR	215
Qy	182	FQYIEGEMRTRIYNRSA	200
Db	216	FQYIEGEMRTRIYNRSA	234

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## OM Protein - protein search, using sw model

Run on: February 10, 2004, 16:18:30 ; Search time 11.5641 seconds  
(without alignments)

Title: US-10-083-336A-10  
Perfect score: 1029  
Sequence: 1 MIFPKQXPPIINFTTAGATVQ.....RFQYIEGEMTRIRVNRRSA 200

Scoring table: BIOSUM62  
Gapext 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters:

326717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database : Issued\_Patents\_AA,\*

- 1: /cgxn2\_6/picodata/1/iaa/5A\_COMB\_pep:\*
- 2: /cgxn2\_6/picodata/1/iaa/5B\_COMB\_pep:\*
- 3: /cgxn2\_6/picodata/1/iaa/6A\_COMB\_pep:\*
- 4: /cgxn2\_6/picodata/1/iaa/6B\_COMB\_pep:\*
- 5: /cgxn2\_6/picodata/1/iaa/PCRV3\_COMB\_pep:\*
- 6: /cgxn2\_6/picodata/1/iaa/backfiles1.DPeP:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	1029	100.0	268	2	US-08-356-786-8	Sequence 8, Appli
2	1029	100.0	534	2	US-08-356-786-10	Sequence 10, Appli
3	1024	99.5	267	1	US-07-301-707-1	Sequence 1, Appli
4	1024	99.5	267	1	US-07-388-430-1	Sequence 1, Appli
5	1024	99.5	267	1	US-08-425-336-1	Sequence 1, Appli
6	1024	99.5	267	1	US-08-488-113-B-1	Sequence 1, Appli
7	1024	99.5	267	1	US-08-646-360-1	Sequence 1, Appli
8	1024	99.5	267	2	US-08-646-360-1	Sequence 1, Appli
9	1024	99.5	267	3	US-08-839-785-1	Sequence 1, Appli
10	1024	99.5	267	3	US-09-136-389-1	Sequence 1, Appli
11	1024	99.5	267	4	US-09-610-838-1	Sequence 1, Appli
12	1024	99.5	267	5	PCN-US99-09487-1	Sequence 1, Appli
13	1024	99.5	290	1	US-08-378-718-A-27	Sequence 27, Appli
14	1024	99.5	290	1	US-08-485-286-27	Sequence 27, Appli
15	1024	99.5	290	6	5248606-4	Patent No. 5248606
16	1014	98.5	267	1	US-08-218-303-16	Sequence 16, Appli
17	1014	98.5	267	1	US-08-338-733D-61	Sequence 61, Appli
18	1014	98.5	267	4	US-09-538-873-1	Sequence 1, Appli
19	934.5	90.8	540	1	US-08-378-761A-77	Sequence 77, Appli
20	934.5	90.8	540	1	US-08-385-286-77	Sequence 77, Appli
21	342	33.2	247	1	US-08-468-113-B-6	Sequence 6, Appli
22	342	33.2	247	1	US-08-477-484-B-6	Sequence 6, Appli
23	342	33.2	247	1	US-08-646-336-6	Sequence 6, Appli
24	342	33.2	247	3	US-08-839-765-6	Sequence 6, Appli
25	342	33.2	247	3	US-09-136-389-6	Sequence 6, Appli
26	342	33.2	247	4	US-09-610-838-6	Sequence 6, Appli
27	342	33.2	267	1	US-08-378-761A-74	Sequence 74, Appli

## ALIGNMENTS

RESULT 1  
US-08-356-786-8  
; Sequence 8, Application US/08356786

; Patent No. 5877305

; GENERAL INFORMATION:  
; APPLICANT: Huston, James S.  
; APPLICANT: Oppermann, Hermann  
; APPLICANT: Houston, L. L.  
; APPLICANT: Ring, David B.  
; TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer  
; TITLE OF INVENTION: Marker  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSE: Edmund R. Pitcher, Testa, Hurwitz, & Thibeault  
; STREET: Exchange Place, 53 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; ZIP: 02109  
; COUNTRY: USA  
; ZIP: 02109  
COMPUTER READABLE FORM:  
; COMPUTER TYPE: Floppy disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release 1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/356,786  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/831,967  
; FILING DATE: 06-FEB-1992  
; ATTORNEY/AGENT INFORMATION:  
; ATTORNEY: Pitcher, Edmund R.  
; REGISTRATION NUMBER: 27,829  
; REFERENCE/DOCKET NUMBER: CRP-053  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 248-7000  
; TELEFAX: (617) 248-7100  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 268 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-356-786-8

Qy 1 MIFPKQPIINFTTAGATVQSYTNFIRAVGRLLTGADVRHEIPVLPNRVGFLPINQRFL 60  
 Db 1 MIFPKQPIINFTTAGATVQSYTNFIRAVGRLLTGADVRHEIPVLPNRVGFLPINQRFL 60  
 Qy 61 VELSNHAELSVTTLADVNAYVGYRAGNSAYFFHPDNOEAAITHLFTDVQNRYTFAF 120  
 Db 61 VELSNHAELSVTTLADVNAYVGYRAGNSAYFFHPDNOEAAITHLFTDVQNRYTFAF 120  
 Qy 121 GNYDRLEQLAGNLRENIELNGNPLEEAISALYYSTGGTQLPTLARSFLICIQMISEAA 180  
 Db 121 GNYDRLEQLAGNLRENIELNGNPLEEAISALYYSTGGTQLPTLARSFLICIQMISEAA 180  
 Qy 181 RFOYIEGMRTRYNRSA 200  
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 RESULT 3  
 US-07-901-707-1  
 ; Sequence 1, Application US/07901707  
 ;  
 GENERAL INFORMATION:  
 ;  
 ; APPLICANT: Bernhard, Susan L.  
 ;  
 ; BETTER, Marc D.  
 ;  
 ; APPLICANT: Carroll, Steve F.  
 ;  
 ; APPLICANT: Lane, Julie A.  
 ;  
 ; TITLE OF INVENTION: Materials Comprising and Methods of  
 ;  
 ; COMPOSITION AND USE FOR Ribosome-Inactivating Proteins  
 ;  
 ; NUMBER OF SEQUENCES: 57  
 ;  
 ; CORRESPONDENCE ADDRESS:  
 ;  
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
 ;  
 ; Bicknell, Street: Two First National Plaza, 20 South Clark  
 ;  
 ; STREET: Street  
 ;  
 ; CITY: Chicago  
 ;  
 ; STATE: Illinois  
 ;  
 ; COUNTRY: USA  
 ;  
 ; ZIP: 60603  
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 ; COMPUTER READABLE FORM:  
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 ; MEDIUM TYPE: Floppy disk  
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 ; COMPUTER: IBM PC compatible  
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 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
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 ; SOFTWARE: Patentin Release #1.0, version #1.25  
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 ; CURRENT APPLICATION DATA:  
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 ; APPLICATION NUMBER: US 07/901,707  
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 ; FILING DATE: 1992-05-19  
 ;  
 ; CLASSIFICATION: 435  
 ;  
 ; PRIOR APPLICATION DATA:  
 ;  
 ; APPLICATION NUMBER: US 07/787,567  
 ;  
 ; FILING DATE: 04-NOV-1991  
 ;  
 ; ATTORNEY/AGENT INFORMATION:  
 ;  
 ; NAME: No. 537546 and, Greta E.  
 ;  
 ; REGISTRATION NUMBER: 35,302  
 ;  
 ; REFERENCE/DOCKET NUMBER: 27129/30910  
 ;  
 ; TELECOMMUNICATION INFORMATION:  
 ;  
 ; TELEPHONE: (312) 346-5750  
 ;  
 ; TELEX: 25-3856  
 ;  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ;  
 ; SEQUENCE CHARACTERISTICS:  
 ;  
 ; LENGTH: 267 amino acids  
 ;  
 ; TYPE: AMINO ACID  
 ;  
 ; TOPOLOGY: linear  
 ;  
 ; MOLECULE TYPE: Protein  
 ;  
 ; US-07-901-707-1  
 ;  
 ; Query Match 99.5%; Score 1024; DB 1; Length 267;  
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 ; Best Local Similarity 100.0%; Pred. No. 8.3e-112; Indels 0; Gaps 0;  
 ;  
 ; Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 ;  
 ; Db 1 IFPKQPIINFTAGATVQSYTNFIRAVGRLLTGADVRHEIPVLPNRVGFLPINQRFL 60  
 ;  
 ; Query 62 ELSNHAELSVTTLADVNAYVGYRAGNSAYFFHPDNOEAAITHLFTDVQNRYTFAF 121  
 ;  
 ; Db 61 ELSNHAELSVTTLADVNAYVGYRAGNSAYFFHPDNOEAAITHLFTDVQNRYTFAF 120  
 ;  
 ; Query 122 GNYDRLEQLAGNLRENIELNGNPLEEAISALYYSTGGTQLPTLARSFLICIQMISEAA 181

Db 121 GNYDRLEQAGNLRENTLNGNPLEEAISALYYSTGGTQLPTLARSFTICQMISEAR 160  
 Qy 182 FQYIEGEMRTRIYNRSA 200  
 Db 181 FQYIEGEMRTRIYNRSA 199

## RESULT 4

US-07-988-430-1  
 ; Sequence 1, Application US/07988430  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bernhard, Susan L.  
 ; BETTER: Marc D.  
 ; APPLICANT: Carroll, Stephen F.  
 ; APPLICANT: Lane, Julie A.  
 ; APPLICANT: Lei, Shau Ping  
 ; TITLE OF INVENTION: Materials Comprising and Methods of Preparation and Use for Ribosome-Inactivating Proteins  
 ; NUMBER OF SEQUENCES: 101  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
 ; ADDRESSEE: Bicknell, Two First National Plaza, 20 South Clark  
 ; STREET: Street  
 ; CITY: Chicago  
 ; STATE: Illinois  
 ; COUNTRY: USA  
 ; ZIP: 60603  
 COMPUTER READABLE FORM:  
 COMPUTER: IBM PC Compatible  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/988,430  
 FILING DATE: 1992-12-09  
 CLASSIFICATION: 435  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 07/901,707  
 FILING DATE: 19-JUN-1992  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 07/787,567  
 FILING DATE: 04-NOV-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: No. 541620 and, Greta E.  
 REGISTRATION NUMBER: 35302  
 REFERENCE/DOCKET NUMBER: 31133  
 FILING DATE: 25-APR-1992  
 TELEPHONE: (312) 346-5750  
 TELEFAX: (312) 984-9740  
 TELEX: 25-3856  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 267 amino acids  
 TYPE: AMINO ACID  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-07-988-430-1

Query Match 99.5%; Score 1024; DB 1; Length 267;  
 Best Local Similarity 100.0%; Fred. No. 8.3e-112;  
 Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 2 IFPKQYIPINFTAGATQSYTNFIRAVRGRLLTGADVRHEIPVNPRLPGLINQRFILY 61  
 Db 1 IFPKQYIPINFTAGATQSYTNFIRAVRGRLLTGADVRHEIPVNPRLPGLINQRFILY 60  
 Qy 62 ELSNHAEISVTIALLDVTNAVYVGYRAGNSAYFHPDNQEDAAITHLFTDVQNRTFAFG 121  
 Db 61 ELSNHAEISVTIALLDVTNAVYVGYRAGNSAYFHPDNQEDAAITHLFTDVQNRTFAFG 120  
 Query Match 99.5%; Score 1024; DB 1; Length 267;  
 Best Local Similarity 100.0%; Pred. No. 8.3e-112;  
 Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 2 IFFPKQYIPINFTAGATQSYTNFIRAVRGRLLTGADVRHEIPVNPRLPGLINQRFILY 61  
 Db 1 IFFPKQYIPINFTAGATQSYTNFIRAVRGRLLTGADVRHEIPVNPRLPGLINQRFILY 60  
 Qy 62 ELSNHAEISVTIALLDVTNAVYVGYRAGNSAYFHPDNQEDAAITHLFTDVQNRTFAFG 121  
 Db 61 ELSNHAEISVTIALLDVTNAVYVGYRAGNSAYFHPDNQEDAAITHLFTDVQNRTFAFG 120  
 Query Match 99.5%; Score 1024; DB 1; Length 267;  
 Best Local Similarity 100.0%; Pred. No. 8.3e-112;  
 Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 2 IFFPKQYIPINFTAGATQSYTNFIRAVRGRLLTGADVRHEIPVNPRLPGLINQRFILY 61  
 Db 1 IFFPKQYIPINFTAGATQSYTNFIRAVRGRLLTGADVRHEIPVNPRLPGLINQRFILY 60  
 Qy 62 ELSNHAEISVTIALLDVTNAVYVGYRAGNSAYFHPDNQEDAAITHLFTDVQNRTFAFG 121  
 Db 61 ELSNHAEISVTIALLDVTNAVYVGYRAGNSAYFHPDNQEDAAITHLFTDVQNRTFAFG 120  
 Query Match 99.5%; Score 1024; DB 1; Length 267;  
 Best Local Similarity 100.0%; Pred. No. 8.3e-112;  
 Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 6

US-08-488-113B-1

Sequence 1, Application US/08488113B

Patent No. 5744590

GENERAL INFORMATION:

APPLICANT: Better, Marc D.

APPLICANT: Carroll, Stephen F.

APPLICANT: Studnicka, Gary M.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins

NUMBER OF SEQUENCES: 169

ADDRESSEE: McAndrews, Held & Malloy, Ltd.

STREET: 500 West Madison Street, 34th Floor

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60661

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/488.113B

FILING DATE: 07-JUN-1995

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 08/064,691

FILING DATE: 12-MAY-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/425,336

FILING DATE: 16-APR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/425,336

FILING DATE: 18-APR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/988,430

FILING DATE: 09-DEC-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/901,707

FILING DATE: 19-JUN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/787,567

FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: McNicholas, Janet M.

REGISTRATION NUMBER: 32,918

REFERENCE/DOCKET NUMBER: 11-022US07/200-70.P3.C2A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/707-8889

TELEFAX: 312/707-9155

TELEX: 650 388-1248

TELEPHONE FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 267 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-488-113B-1

Query Match Similarity 99.5%; Score 1024; DB 1; Length 267;

Best Local Similarity 100.0%; Pred. No. 8.3e-112; Length 267;

Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IFPKQYPIINFTTAGATQSYTNFRAVRGRLTGADVRHEIPVLPNRGLPINQRFIVL 61

Db 1 IFPKQYPIINFTTAGATQSYTNFRAVRGRLTGADVRHEIPVLPNRGLPINQRFIVL 60

Qy 62 ELSNHAEISVTIADVTNAYTGYRACNSAYEFFHDQNQEDAITHLFFDQNYRTFAFG 121

Db 61 ELSNHAEISVTIADVTNAYTGYRACNSAYEFFHDQNQEDAITHLFFDQNYRTFAFG 120

Qy 122 GNYDRLEQAGLNRENTLGNGPLEEAISALYYSTGGTQLPTLARSFIICQMISEAR 181

Db 121 GNYDRLEQAGLNRENTLGNGPLEEAISALYYSTGGTQLPTLARSFIICQMISEAR 180

RESULT 7

US-08-477-484B-1

Sequence 1, Application US/08477484B

Patent No. 5756699

GENERAL INFORMATION:

APPLICANT: Better, Marc D.

APPLICANT: Carroll, Stephen F.

APPLICANT: Studnicka, Gary M.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins

NUMBER OF SEQUENCES: 169

CORRESPONDENCE ADDRESS:

ADDRESSEE: McAndrews, Held & Malloy, Ltd.

STREET: 500 West Madison Street, 34th floor

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60661

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/477,484B

FILING DATE: 07-JUN-1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/425,336

FILING DATE: 16-APR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/901,707

FILING DATE: 12-MAY-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/988,430

FILING DATE: 09-DEC-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/901,707

FILING DATE: 19-JUN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/787,567

FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: McNicholas, Janet M.

REGISTRATION NUMBER: 32,918

REFERENCE/DOCKET NUMBER: 11-022US07/200-70.P3.C2A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/707-8889

TELEFAX: 312/707-9155

TELEX: 650 388-1248

TELEPHONE FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 267 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-477-484B-1

Query Match Similarity 99.5%; Score 1024; DB 1; Length 267;

Best Local Similarity 100.0%; Pred. No. 8.3e-112; Length 267;

Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 182 FOYIEGMRTRIYNRS 200

Db 181 FOYIEGMRTRIYNRS 199

Qy 182 FOYIEGMRTRIYNRS 200

Db 181 FOYIEGMRTRIYNRS 199

Best Local Similarity 100.0%; Pred. No. 8.3e-112; Mismatches 0; Indels 0; Gaps 0;

Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-646-360-1

Query Match 99.5%; Score 1024; DB 2; Length 267;  
Best Local Similarity 100.0%; Pred. No. 8.3e-112;  
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IFPKQYPIINFATGATVQSYTFNIRAVRGRLLTGADRVHEIPVLPNRVLGLINQRFILV 61  
Db 1 IFPKQYPIINFATGATVQSYTFNIRAVRGRLLTGADRVHEIPVLPNRVLGLINQRFILV 60

Qy 62 ELSNHAEELSVTLALDVTNAAYVGYRAGNSAYFFPDNOEDAFAITHLFTDVQNYRTFAFG 121  
Db 61 ELSNHAEELSVTLALDVTNAAYVGYRAGNSAYFFPDNOEDAFAITHLFTDVQNYRTFAFG 120

Qy 122 GNYDRLEQLAGNLRENTLGNGPLEEAISALYYSTGGTQPLTLARSFICIQMISEAAR 181  
Db 121 GNYDRLEQLAGNLRENTLGNGPLEEAISALYYSTGGTQPLTLARSFICIQMISEAAR 180

Qy 182 FOYIEGEMTRTRYNRSA 200  
Db 181 FOYIEGEMTRTRYNRSA 199

RESULT 8  
US-08-646-360-1  
Sequence 1 Application US/08646360  
Patent No. 5837491  
GENERAL INFORMATION:  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Better, Marc D.  
APPLICANT: Studnik, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
NUMBER OF SEQUENCES: 173  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th Floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,360  
FILING DATE: 13-MAY-1996  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/05348  
FILING DATE: 12-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/998,430  
FILING DATE: 09-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE DOCKET NUMBER: 20-0-70.P4  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
SEQUENCE CHARACTERISTICS:  
LENGTH: 267 amino acids

---

RESULT 9  
US-08-839-765-1  
Sequence 1 Application US/08839765  
Patent No. 6146631  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studnik, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
NUMBER OF SEQUENCES: 169  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/839,765  
FILING DATE: 15-APR-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/425,336  
FILING DATE: 18-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/0839,765  
FILING DATE: 12-MAY-1993  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE DOCKET NUMBER: 20-0-70.P4  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
SEQUENCE CHARACTERISTICS:  
LENGTH: 267 amino acids

TELEPHONE: 312/707-8889  
 TELEFAX: 312/707-9155  
 TELELEX: 650 388-1248  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 267 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-839-765-1;

Query Match 99.5%; Score 1024; DB 3; Length 267;  
 Best Local Similarity 100.0%; Pred. No. 8.3e-112;  
 Matches 199; Conservative 0; N mismatches 0; Indels 0; Gaps 0;

Qy 2 IFPKQYPIINFTAGATVQSYTNFTRAVGRGLTGSADVRHEIPVLPNRVGLPINQRFLIV 61  
 Db 1 IFPKQYPIINFTAGATVQSYTNFTRAVGRGLTGSADVRHEIPVLPNRVGLPINQRFLIV 60

Qy 62 ELSNHAEISVTLLADTVTAATVYVGDRAGNSAYFFHDNQDAEAITHLFDVQNYRTFAFG 121  
 Db 61 ELSNHAEISVTLLADTVTAATVYVGDRAGNSAYFFHDNQDAEAITHLFDVQNYRTFAFG 120

Qy 122 GNYDRLQLAGNLRENIELGNGPLEEAISSAYYYSTGGTQLPTLARSFLICIONISEAR 181  
 Db 121 GNYDRLQLAGNLRENIELGNGPLEEAISSAYYYSTGGTQLPTLARSFLICIONISEAR 180

Qy 182 FQYIEGEMTRIYRNRS 200  
 Db 181 FQYIEGEMTRIYRNRS 199

RESULT 10  
 US-03-136-389-1  
 Sequence 1, Application US/09136389  
 Patent No. 6146850  
 GENERAL INFORMATION:  
 APPLICANT: Better, Marc D.  
 APPLICANT: Carroll, Stephen F.  
 APPLICANT: Studnka, Gary M.  
 TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
 NUMBER OF SEQUENCES: 173  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
 STREET: 500 West Madison Street, 34th floor  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: USA  
 ZIP: 60661  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/136,389  
 FILING DATE:  
 CLASSIFICATION:  
 PRIORITY DATA:  
 APPLICATION NUMBER: US 07/988,430  
 FILING DATE: 09-DEC-1992  
 PRIORITY DATA:  
 APPLICATION NUMBER: US 07/901,707  
 FILING DATE: 19-JUN-1992

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/787,567  
 FILING DATE: 04-NOV-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: McNicholas, Janet M.  
 REGISTRATION NUMBER: 32,918  
 REFERENCE/DOCKET NUMBER: 200-70.P4  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 312/707-8889  
 TELEFAX: 312/707-9155  
 TELEX: 650 388-1248  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 267 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-136-389-1;

Query Match 99.5%; Score 1024; DB 3; Length 267;  
 Best Local Similarity 100.0%; Pred. No. 8.3e-112;  
 Matches 199; Conservative 0; N mismatches 0; Indels 0; Gaps 0;

Qy 2 IFPKQYPIINFTAGATVQSYTNFTRAVGRGLTGSADVRHEIPVLPNRVGLPINQRFLIV 61  
 Db 1 IFPKQYPIINFTAGATVQSYTNFTRAVGRGLTGSADVRHEIPVLPNRVGLPINQRFLIV 60

Qy 62 ELSNHAEISVTLLADTVTAATVYVGDRAGNSAYFFHDNQDAEAITHLFDVQNYRTFAFG 121  
 Db 61 ELSNHAEISVTLLADTVTAATVYVGDRAGNSAYFFHDNQDAEAITHLFDVQNYRTFAFG 120

Qy 122 GNYDRLQLAGNLRENIELGNGPLEEAISSAYYYSTGGTQLPTLARSFLICIONISEAR 181  
 Db 121 GNYDRLQLAGNLRENIELGNGPLEEAISSAYYYSTGGTQLPTLARSFLICIONISEAR 180

Qy 182 FQYIEGEMTRIYRNRS 200  
 Db 181 FQYIEGEMTRIYRNRS 199

RESULT 11  
 US-03-610-838-1  
 Sequence 1, Application US/09610838  
 Patent No. 6376217  
 GENERAL INFORMATION:  
 APPLICANT: Better, Marc D.  
 APPLICANT: Carroll, Stephen F.  
 APPLICANT: Studnka, Gary M.  
 TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
 NUMBER OF SEQUENCES: 173  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
 STREET: 500 West Madison Street, 34th floor  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: USA  
 ZIP: 60661  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/610,838  
 FILING DATE: 06-JUL-2000  
 CLASSIFICATION:  
 PRIORITY DATA:  
 APPLICATION NUMBER: US/09/136,389  
 FILING DATE: 18-AUG-1998  
 APPLICATION NUMBER: 08/646,360  
 FILING DATE: 13-JAY-1996  
 APPLICATION NUMBER: PCT/US94/05348  
 FILING DATE: 19-JUN-1992

FILING DATE: 12-MAY-1994  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/064,691  
 FILING DATE: 12-MAY-1993  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 07/988,430  
 FILING DATE: 09-DEC-1992  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 07/901,707  
 FILING DATE: 19-JUN-1992  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 07/787,567  
 FILING DATE: 04-NOV-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: McNicholas, Janet M.  
 REGISTRATION NUMBER: 32,918  
 REFERENCE/DOCKET NUMBER: 200-70.P4  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 312/707-8889  
 TELEX: 650 38-1248  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 267 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-03-610-838-1

Query Match 99.5%; Score 1024; DB 4; Length 267;  
 Best Local Similarity 100.0%; Pred. No. 8.3e-112;  
 Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 2 IIPKQYPIINFTAGATQSYTNFIRAVRGRITTGADVRHEIPVLPNVRGLPINQRFILV 61  
 Db 1 IIPKQYPIINFTAGATQSYTNFIRAVRGRITTGADVRHEIPVLPNVRGLPINQRFILV 60  
 Qy 62 ELSNHAEIISVTIADLVNTAAYVGYRAGNSAYFHPDNQEDAITHLFTDVQNRYTFAGF 121  
 Db 61 ELSNHAEIISVTIADLVNTAAYVGYRAGNSAYFHPDNQEDAITHLFTDVQNRYTFAGF 120  
 Qy 122 GNYDRLEQLAGNLRENTIELNGNPLEEASALYYSTGGTOLPLTLARSFIICIQMISEAR 181  
 Db 121 GNYDRLEQLAGNLRENTIELNGNPLEEASALYYSTGGTOLPLTLARSFIICIQMISEAR 180  
 Qy 182 FQYIEGEMRTRTRYNRS 200  
 Db 181 FQYIEGEMRTRTRYNRS 199

RESULT 12  
 PCT-US92-09487-1  
 Sequence 1, Application PC/TUS9209487  
 GENERAL INFORMATION:  
 APPLICANT: Bernhard, Susan L.  
 APPLICANT: Better, Marc D.  
 APPLICANT: Carroll, Stephen F.  
 APPLICANT: Lane, Julie A.  
 APPLICANT: Lei, Shau-Ping  
 TITLE OF INVENTION: Materials Comprising and Methods of Preparation and Use for Ribosome-Inactivating Proteins  
 NUMBER OF SEQUENCES: 101  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
 ADDRESSEE: Bicknell  
 STREET: Two First National Plaza, 20 South Clark  
 STREET: Street  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: USA  
 ZIP: 60603  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk

RESULT 13  
 US-08-378-761A-27  
 Sequence 27, Application US/08378761A  
 Patent No. 5535384  
 GENERAL INFORMATION:  
 APPLICANT: WALSH, TERENCE A  
 APPLICANT: HEY, TIMOTHY D  
 APPLICANT: MORGAN, ALICE ER  
 TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE  
 TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF  
 NUMBER OF SEQUENCES: 81  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: ANDREA T. BORUCKI  
 STREET: 9330 ZIONSVILLE ROAD  
 CITY: INDIANAPOLIS  
 STATE: IN  
 COUNTRY: US  
 ZIP: 46268  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/378,761A  
 FILING DATE: 26-JAN-1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BORUCKI, ANDREA T  
 REGISTRATION NUMBER: 33651  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (317) 337-4846  
 INFORMATION FOR SEQ ID NO: 27:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 290 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-378-761A-27

Query Match 99.5%; Score 1024; DB 1; Length 290;  
 Best Local Similarity 100.0%; Pred. No. 9.4e-112;  
 Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IFPKQYPIINFTAGATVQSYTNFRAVRGELTGTADVRHEIPVLPNRYGLPINQRFLV 61  
 Db 25 IFPKQYPIINFTAGATVQSYTNFRAVRGELTGTADVRHEIPVLPNRYGLPINQRFLV 84

Qy 62 ELSNHAEALSVTLLADTVNAYVGYRAGNSAYFFHPDQEDAETHLFTDVQNYTFAFG 121  
 Db 85 ELSNHAEALSVTLLADTVNAYVGYRAGNSAYFFHPDQEDAETHLFTDVQNYTFAFG 144

Qy 122 GNYDRLEQLAGNLRENTIELNGPLEEAISALYYSTGGTOLPLARSFICTIONISEAR 181  
 Db 145 GNYDRLEQLAGNLRENTIELNGPLEEAISALYYSTGGTOLPLARSFICTIONISEAR 204

Qy 182 FOYIEGEMTRIRYNRSA 200  
 Db 205 FOYIEGEMTRIRYNRSA 223

RESULT 15  
 5248606-4

;Patent No. 5248606  
 ;APPLICANT: WALSH, TERENCE A.;HEY, TIMOTHY D.;MORGAN,  
 ;NAME: ALICE E.R.  
 ;TITLE OF INVENTION: DNA ENCODING INACTIVE PRECURSOR AND  
 ;ACTIVE FORMS OF MAIZE RIBOSOME INACTIVATING  
 ;SEQUENCES: 49  
 ;NUMBER OF SEQUENCES: 49  
 ;CURRENT APPLICATION DATA:  
 ;APPLICATION NUMBER: US/07/535,636  
 ;FILING DATE: 11-JUN-1990  
 ;SEQ ID NO:4;  
 ;LENGTH: 290

Query Match 99.5%; Score 1024; DB 6; Length 290;

Best Local Similarity 100.0%; Pred. No. 9.4e-112;  
 Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IFPKQYPIINFTAGATVQSYTNFRAVRGELTGTADVRHEIPVLPNRYGLPINQRFLV 61  
 Db 25 IFPKQYPIINFTAGATVQSYTNFRAVRGELTGTADVRHEIPVLPNRYGLPINQRFLV 84

Qy 62 ELSNHAEALSVTLLADTVNAYVGYRAGNSAYFFHPDQEDAETHLFTDVQNYTFAFG 121  
 Db 85 ELSNHAEALSVTLLADTVNAYVGYRAGNSAYFFHPDQEDAETHLFTDVQNYTFAFG 144

Qy 122 GNYDRLEQLAGNLRENTIELNGPLEEAISALYYSTGGTOLPLARSFICTIONISEAR 181  
 Db 145 GNYDRLEQLAGNLRENTIELNGPLEEAISALYYSTGGTOLPLARSFICTIONISEAR 204

Qy 182 FOYIEGEMTRIRYNRSA 200  
 Db 205 FOYIEGEMTRIRYNRSA 223

Search completed: February 10, 2004, 16:29:35

Sun Feb 15 07:29:55 2004

us-10-083-336a-10.ra1

Page 9

Job time : 12.5641 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 10, 2004, 16:26:46 ; Search time 25.7969 Seconds  
 (without alignments)  
 1623.314 Million cell updates/sec

Title: US-10-083-336A-10  
 Perfect score: 1029  
 Sequence: MIFPKQIPIINFTAGATVQ.....RFQYIEGMRTRIYNSA 200

Scoring table: BLOSUM62  
 Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**ALIGNMENTS**

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3	1024	99.5	267	12	US-10-127-890-1	Sequence 1, Appli	
4	1024	99.5	576	12	US-10-083-336A-1	Sequence 1, Appli	
5	1020	99.1	198	12	US-10-083-336A-3	Sequence 3, Appli	
6	1014	98.5	267	12	US-10-282-935-1	Sequence 1, Appli	
7	1014	98.5	267	12	US-10-040-798-1	Sequence 7, Appli	
8	1010	98.2	198	12	US-10-083-336A-7	Sequence 11, Appli	
9	960	93.3	190	12	US-10-083-336A-11	Sequence 6, Appli	
10	956	92.9	189	12	US-10-083-336A-6	Sequence 4, Appli	
11	951	92.4	188	12	US-10-083-336A-4	Sequence 8, Appli	
12	941	91.4	188	12	US-10-083-336A-8	Sequence 9, Appli	
13	934.5	90.8	185	12	US-10-083-336A-9	Sequence 2, Appli	
14	748	72.7	179	12	US-10-083-336A-2	Sequence 39, Appli	
15	342	33.2	247	12	US-10-127-890-6	Sequence 2, Appli	
16	342	33.2	247	12	US-10-375-209A-39	Sequence 4, Appli	
17	342	33.2	289	12	US-10-280-679B-4	Sequence 3, Appli	
18	342	33.2	251	12	US-10-282-935-3	Sequence 34, Appli	
19	323.5	31.4	251	12	US-10-440-796-3	Sequence 34, Appli	
20	323.5	31.4	247	10	US-09-792-793A-34	Sequence 4, Appli	
21	312	30.3	247	12	US-10-375-209A-34	Sequence 7, Appli	
22	312	30.3	263	12	US-10-127-890-4	Sequence 2, Appli	
23	279	26.9	252	9	US-09-347-064-2	Sequence 8, Appli	
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25	276	26.8	248	12	US-10-127-890-5	Sequence 5, Appli	
26	276	26.8	251	12	US-10-127-890-110	Sequence 11, App	
27	267.5	26.0	24.1	251	12	US-10-127-890-101	Sequence 10.1, App
28	249.5	24.2	24.0	251	12	US-10-127-890-107	Sequence 10.6, App
29	249.5	24.2	24.0	251	9	US-09-765-527-247	Sequence 247, App
30	248.5	24.1	23.9	251	12	US-10-127-890-2	Sequence 2, Appli
31	247.5	24.1	24.1	251	12	US-10-127-890-19	Sequence 99, Appli
32	247.5	24.1	24.1	251	12	US-10-127-890-103	Sequence 107, App
33	246.5	24.0	24.0	251	12	US-10-127-890-104	Sequence 100, App
34	246.5	24.0	23.9	251	12	US-10-127-890-105	Sequence 105, App
35	245.5	23.9	23.9	316	12	US-10-074-596-1	Sequence 11, Appli
36	245.5	23.9	23.9	507	12	US-10-074-596-11	Sequence 259, App
37	245.5	23.9	23.9	322	9	US-09-765-527-259	Sequence 253, App
38	245.5	23.9	23.9	332	9	US-09-765-527-253	Sequence 251, App
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**RESULT 1**  
 US-10-083-336A-10  
 ; Sequence 10, Application US/10083336A  
 ; Publication No. US2003018165AA1

**GENERAL INFORMATION:**  
 ; APPLICANT: Olson, Mark A  
 ; MILLARD, Charles B  
 ; BYRNE, Michael P  
 ; WAMMACHER, Robert W  
 ; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof  
 ; FILE REFERENCE: P6745USD (RIID 01-58)  
 ; CURRENT APPLICATION NUMBER: US/10/083,336A  
 ; FILING DATE: 2002-05-21  
 ; NUMBER OF SEQ ID NOS: 15  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO: 10  
 ; LENGTH: 200  
 ; TYPE: PRT  
 ; ORGANISM: Ricinus communis  
 US-10-083-336A-10

**SUMMARIES**

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Result No.	Score	Query	Match	Length	DB ID	Description
1	1029	100.0	200	12	US-10-083-336A-10	Sequence 10, Appli
2	1025	99.6	199	12	US-10-083-336A-5	Sequence 5, Appli
3	1024	99.5	267	12	US-10-127-890-1	Sequence 1, Appli
4	1024	99.5	576	12	US-10-083-336A-1	Sequence 1, Appli
5	1020	99.1	198	12	US-10-083-336A-3	Sequence 3, Appli
6	1014	98.5	267	12	US-10-282-935-1	Sequence 1, Appli
7	1014	98.5	267	12	US-10-040-798-1	Sequence 7, Appli
8	1010	98.2	198	12	US-10-083-336A-7	Sequence 11, Appli
9	960	93.3	190	12	US-10-083-336A-11	Sequence 6, Appli
10	956	92.9	189	12	US-10-083-336A-6	Sequence 4, Appli
11	951	92.4	188	12	US-10-083-336A-4	Sequence 8, Appli
12	941	91.4	188	12	US-10-083-336A-8	Sequence 9, Appli
13	934.5	90.8	185	12	US-10-083-336A-9	Sequence 2, Appli
14	748	72.7	179	12	US-10-083-336A-2	Sequence 39, Appli
15	342	33.2	247	10	US-09-792-793A-39	Sequence 39, Appli

**Query Match** 100.0%; Score 1029; DB 12; Length 200;  
**Best Local Similarity** 100.0%; **Indels** 0; **Gaps** 0;  
**Matches** 200; **Mismatches** 0;

Qy 1 MIFPKQYPINFTAGATVQSYNTNFTRAVRGRLTGADVRHEIPVLPNVLGLPINORFIL 60  
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Qy 1 VELSNHAELSVTLALDVTVNAYVGYRAGNSAYFFHDNQEDAEATHLFTDYNQRYTEAF 120  
 Db 61 VELSNHAELSVTLALDVTVNAYVGYRAGNSAYFFHDNQEDAEATHLFTDYNQRYTEAF 120

Qy 121 GGNYDRLEQLAGNLRENIELGNGPLEEASLYYYSTGGTQLPLTARSFLICQIMSEAA 180  
 Db 121 GGNYDRLEQLAGNLRENIELGNGPLEEASLYYYSTGGTQLPLTARSFLICQIMSEAA 180

Qy 181 RFQYIEGMRTRIYRNRSAA 200

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/646,360  
 FILING DATE: 13-MAY-1996  
 APPLICATION NUMBER: PCT/US94/05348  
 FILING DATE: 12-MAY-1994  
 APPLICATION NUMBER: US 08/064,691  
 FILING DATE: 12-MAY-1993  
 APPLICATION NUMBER: US 07/988,430  
 FILING DATE: 09-DEC-1992  
 APPLICATION NUMBER: US 07/901,707  
 FILING DATE: 19-JUN-1992  
 APPLICATION NUMBER: US 07/787,567  
 FILING DATE: 04-NOV-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Monicholas, Janet M.  
 REGISTRATION NUMBER: 32,918  
 REFERENCE/DOCKET NUMBER: 200-70-P4  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 312/707-8889  
 TELEX: 312/707-9155  
 FAX: 312/707-1248  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 267 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: Protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
 US-10-127-890-1

Query Match 99.5%; Score 1024; DB 12; Length 267;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-109;  
 Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MIFPKOPIINFTAGATVQSYTNFIAVRGLITGADYRHEIPVLPNVRGLPINQRFL 60  
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Qy 61 VELSHAEILSTVLADVTNAVVGTRAGNSAYFFPDNQDAEATHLFDVQRYTFAF 120  
 Db 61 VELSHAEILSTVLADVTNAVVGTRAGNSAYFFPDNQDAEATHLFDVQRYTFAF 120

Qy 121 GGNYDRLEQLAGNLRNIELNGNPLEEAISALYYSTGGTQLPTLARSFLICIQMISEAR 180  
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Qy 181 RFQYEGEMTRIRYRNRS 199  
 Db 181 RFQYEGEMTRIRYRNRS 199

RESULT 3  
 US-10-127-890-1  
 Sequence 1, Application US/10127890  
 Publication No. US20030166196A1

GENERAL INFORMATION:  
 APPLICANT: Better, Marc D.  
 Carroll, Stephen F.  
 STUDIKA, Gary M.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins

NUMBER OF SEQUENCES: 173

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
 STREET: 500 West Madison Street, 34th Floor  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: USA  
 ZIP: 60661

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/127,890  
 FILING DATE: 23-Apr-2002  
 CLASSIFICATION: <Unknown>

RESULT 4  
 US-10-083-336A-1  
 Sequence 1, Application US/10083336A  
 Publication No. US 030181665A1

GENERAL INFORMATION:  
 APPLICANT: Olson, Mark A.  
 APPLICANT: Millard, Charles B  
 APPLICANT: Byrne, Michael P  
 APPLICANT: Wannemacher, Robert W  
 TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof  
 FILE REFERENCE: P6742US0 (RIRD 01-58)  
 CURRENT APPLICATION NUMBER: US/10/083,336A  
 CURRENT FILING DATE: 2002-05-21  
 NUMBER OF SEQ ID NOS: 15  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO: 1  
 LENGTH: 576  
 TYPE: PRT  
 ORGANISM: Ricinus communis  
 US-10-083-336A-1

Query Match 99.5%; Score 1024; DB 12; Length 576;

Best Local Similarity 100.0%; Pred. No. 1e-108; Mismatches 0; Indels 0; Gaps 0;  
 Matches 199; Conservative 0; Feature: Peptide

Qy 2 IPKKQPIINFTAGATQSYTNFIRAVRGRITGADVRHEIPVLPNVLGINORFILY 61  
 Db 36 IPKQYPIINFTAGATQSYTNFIRAVRGRITGADVRHEIPVLPNVLGINORFILY 95  
 Qy 62 ELSNHAEALSTVLAIDVNTAAYVGYRAGNSAYFHPDNQEDAIAITHLFTDVQNRYTFARG 121  
 Db 96 ELSNHAEALSTVLAIDVNTAAYVGYRAGNSAYFHPDNQEDAIAITHLFTDVQNRYTFARG 155  
 Qy 122 GNYDRLQLAGNLRENIELNGPLEEALSAIYYSTGGTOLPTLARSFIICQMISEAAR 181  
 Db 156 GNYDRLQLAGNLRENIELNGPLEEALSAIYYSTGGTOLPTLARSFIICQMISEAAR 215  
 Qy 182 FQYIEGMRTRIYNRSA 200  
 Db 216 FQYIEGMRTRIYNRSA 234

RESULT 5 US-10-083-336A-3  
 ; Sequence 3, Application US/10083336A  
 ; Publication No. US20030181665A1  
 ; GENERAL INFORMATION  
 ; APPLICANT: Olson, Mark A.  
 ; APPLICANT: Millard, Charles B.  
 ; APPLICANT: Byrne, Michael P.  
 ; APPLICANT: Wannemacher, Robert W.  
 ; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof  
 ; FILE REFERENCE: P6745US0 (RIID 01-58)  
 ; CURRENT APPLICATION NUMBER: US/10/083,336A  
 ; CURRENT FILING DATE: 2002-05-21  
 ; NUMBER OF SEQ ID NOS: 15  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO: 3  
 ; LENGTH: 198  
 ; TYPE: PRT  
 ; ORGANISM: Ricinus communis

US-10-083-336A-3  
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 Matches 198; Conservative 0; Feature: Peptide

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 Qy 122 GNYDRLQLAGNLRENIELNGPLEEALSAIYYSTGGTOLPTLARSFIICQMISEAAR 181  
 Db 121 GNYDRLQLAGNLRENIELNGPLEEALSAIYYSTGGTOLPTLARSFIICQMISEAAR 180  
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 Db 181 FQYIEGMRTRIYNRSA 198

RESULT 7 US-10-440-796-1

; Sequence 1, Application US/10440796  
 ; Publication No. US2004009148A1  
 ; GENERAL INFORMATION  
 ; APPLICANT: VITETTA, ELLEN S.  
 ; APPLICANT: GHETIE, VICTOR F.  
 ; APPLICANT: SMALLISHAW, JOAN  
 ; APPLICANT: BALUNA, ROXANA G.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR AMELIORATING VASCULAR LEAK  
 ; FILE REFERENCE: US/10/440-796-1  
 ; CURRENT APPLICATION NUMBER: US/10/440-796-1  
 ; CURRENT FILING DATE: 2003-05-19  
 ; PRIOR APPLICATION NUMBER: US/09-538,873  
 ; PRIOR FILING DATE: 2000-03-30  
 ; PRIOR APPLICATION NUMBER: 60/126,826  
 ; PRIOR FILING DATE: 1999-03-30  
 ; NUMBER OF SEQ ID NOS: 19  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO: 1  
 ; LENGTH: 267  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence

Query Match 98.5%; Score 1014; DB 12; Length 267;  
 Best Local Similarity 100.0%; Pred. No. 4.8e-108;  
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 3 PKQYPIINFTAGATQSYTNFIRAVRGRITGADVRHEIPVLPNVLGINORFILY 62  
 Qy 64 SNAHAEALSTVLAIDVNTAAYVGYRAGNSAYFHPDNQEDAIAITHLFTDVQNRYTFARG 123  
 Db 63 SNAHAEALSTVLAIDVNTAAYVGYRAGNSAYFHPDNQEDAIAITHLFTDVQNRYTFARG 122  
 Qy 124 YDRLEOLAGNLRENIELNGPLEEALSAIYYSTGGTOLPTLARSFIICQMISEAARFQ 183  
 Db 123 YDRLEOLAGNLRENIELNGPLEEALSAIYYSTGGTOLPTLARSFIICQMISEAARFQ 182  
 Qy 184 YIEGENMRTRIYNRSA 200  
 Db 183 YIEGENMRTRIYNRSA 199

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; SEQ ID NO: 11
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A:11

Query Match          93.3%; Score 960; DB 12; Length 190;
Best Local Similarity 95.0%; Pred. No. 4.8e-102;
Matches 190; Conservative 0; Mismatches 0; Indels 10; Gaps 1;
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Db      1 MIFPKQPIINFTAGATVOSYNTNFTRAVGRLT-----VLPNRVGLPINKQRFL 50
;
Qy      61 VELSNHAELSVTLALDVNTNAYVVGYRAGNSAYFFHDQNQDEAITHLFTDQNRYTFAF 120
Db      51 VELSNHAELSVTLALDVNTNAYVVGYRAGNSAYFFHDQNQDEAITHLFTDQNRYTFAF 110
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Qy      121 GGNYDRLEQLAGNLRENIELNGNPLEAISALYYSTGGTQLPTLARSFTICIQMSEAA 180
Db      111 GGNYDRLEQLAGNLRENIELNGNPLEAISALYYSTGGTQLPTLARSFTICIQMSEAA 170
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Qy      181 RFQYIEGEMRTRIYNRS 200
Db      171 RFQYIEGEMRTRIYNRS 190
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RESULT 10
US-10-083-336A-6
; Sequence 6, Application US/10083336A
; Publication No. US2003018165A1
; GENERAL INFORMATION;
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannenbach, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 6
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A:6

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Matches 189; Conservative 0; Mismatches 0; Indels 10; Gaps 1;
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Db      1 MIFPKQPIINFTAGATVOSYNTNFTRAVGRLT-----VLPNRVGLPINKQRFL 50
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Qy      61 VELSNHAELSVTLALDVNTNAYVVGYRAGNSAYFFHDQNQDEAITHLFTDQNRYTFAF 120
Db      51 VELSNHAELSVTLALDVNTNAYVVGYRAGNSAYFFHDQNQDEAITHLFTDQNRYTFAF 110
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Qy      121 GGNYDRLEQLAGNLRENIELNGNPLEAISALYYSTGGTQLPTLARSFTICIQMSEAA 180
Db      111 GGNYDRLEQLAGNLRENIELNGNPLEAISALYYSTGGTQLPTLARSFTICIQMSEAA 170
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Qy      181 RFQYIEGEMRTRIYNRS 199
Db      171 RFQYIEGEMRTRIYNRS 189
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RESULT 11
US-10-083-336A-4
; Sequence 4, Application US/10083336A
; Publication No. US2003018165A1

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GENERAL INFORMATION:							
APPLICANT:	Olson, Mark A						
APPLICANT:	Millard, Charles B						
APPLICANT:	Byrne, Michael P						
APPLICANT:	Wannemacher, Robert W						
TITLE OF INVENTION:	Ricin Vaccine and Methods of Making and Using Thereof						
FILE REFERENCE:	P67452US0 (RIID 01-58)						
CURRENT APPLICATION NUMBER:	US/10/083,336A						
CURRENT FILING DATE:	2002-05-21						
NUMBER OF SEQ ID NOS:	15						
SOFTWARE:	PatentIn Ver. 2.1						
SEQ ID NO	4						
LENGTH:	188						
TYPE:	PRT						
ORGANISM:	Ricinus communis						
SEQ-10-083-336A-4							
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	Best Local Similarity 94.9%	Pred. No. 5.1e-101;					
	Matches 188; Conservative 0;	Mismatches 0;	Indels 10;	Gaps			
Qy	2 IPKQYPIINFATGATVQSYTNTFTRAVGRGLTCAVDVRHEIPVLPNRYGLPINCORFILVY 61						
Db	1 IPKQYPIINFATGATVQSYTNTFTRAVGRILTCAVDVRHEIPVLPNRYGLPINCORFILVY 50						
Qy	62 ELSNAEISVTLALDVINAYVVGAGRNSAYFFHDNOEAEATHLFTDQNRYTFAGC 122						
Db	51 ELSNAEISVTLALDVINAYVVGAGRNSAYFFHDQEAEATHLFTDQNRYTFAGC 111						
Qy	122 GNYDPLQLAGNLRENIELNGNPFLFAISALYYSTGGTQLPTLARSFIIICIQMISEAR 18						
Db	111 GNYDPLQLAGNLRENIELNGNPFLFAISALYYSTGGTQLPTLARSFIIICIQMISEAR 17						
Qy	182 FQYIEGEAFTIRYRNRRS 199						
Db	171 FQYIEGEAFTIRYRNRRS 188						
RESULT 12 SEQ-10-083-336A-8							
Qy	Sequence 8, Application US/10083336A						
	Publication No. US20030181665A1						
Qy	GENERAL INFORMATION:						
	APPLICANT: Olson, Mark A						
	APPLICANT: Millard, Charles B						
	APPLICANT: Byrne, Michael P						
	APPLICANT: Wannemacher, Robert W						
	TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof						
	FILE REFERENCE: P67452US0 (RIID 01-58)						
	CURRENT APPLICATION NUMBER: US/10/083,336A						
	CURRENT FILING DATE: 2002-05-21						
	NUMBER OF SEQ ID NOS:	15					
	SOFTWARE:	PatentIn Ver. 2.1					
	SEQ ID NO	8					
	LENGTH:	188					
	TYPE:	PRT					
	ORGANISM:	Ricinus communis					
SEQ-10-083-336A-8							
Qy	Query Match	Score 91.4%	DB 12;	Length 188;			
	Best Local Similarity 94.9%	Pred. No. 7.2e-100;					
	Matches 186; Conservative 0;	Mismatches 0;	Indels 10;	Gaps			
Qy	4 PRQYPIINFATGATVQSYTNTFTRAVGRGLTCAVDVRHEIPVLPNRYGLPINCORFILV 63						
Db	3 PRQYPIINFATGATVQSYTNTFTRAVGRILTCAVDVRHEIPVLPNRYGLPINCORFILV 52						
Qy	64 SNHAEISVTLALDVINAYVVGAGRNSAYFFHDNOEAEATHLFTDQNRYTFAGC 122						
Db	53 SNHAEISVTLALDVINAYVVGAGRNSAYFFHDQEAEATHLFTDQNRYTFAGC 111						
Qy	124 YDRLEQAGNLRENIELNGNPFLFAISALYYSTGGTQLPTLARSFIIICIQMISEAR 18						

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RESULTS 13
US-10-083-336A-9
; Sequence 9, Application US/10083336A
; Publication No. US2003018165A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RID 01-58)
; CURRENT APPLICATION NUMBER: US710/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 9
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-9

Query Match          90.8%; Score 934.5; DB 12; Length 185;
Best Local Similarity 93.4%; Pred. No. 3.9e-99; Index 13; Gaps 1;
Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

QY  2 1PFPKQYPINFTAGATVQSYTNFIRAVRGRLLTGADVRHIEPVLPNRYGLPINQRFLV 61
DB   1 1PFPKQYPINFTAGATVQSYTNFIRAVRGRLL-----NRVGLPINQRFLV 47

QY  62 ELSNHAEISVTLLDVTNAVYVGYRAGNSAYFFPHQNQDEAAITLFLTDVNQRTTFAFG 121
DB   48 ELSNHAEISVTLLDVTNAVYVGYRAGNSAYFFPHQNQDEAAITLFLTDVNQRTTFAFG 107

QY  122 GTYDRLEQAGLNIRENLNGPLEEAISALYYSTGGTOLPLTARSFIICLQMISAA 181
DB   108 GNDRLEQAGNIRENLNGPLEEAISALYYSTGGTOLPLTARSFIICLQMISAA 167

QY  182 FOXIEGEMRTRIYNRRS 199
DB   168 FOXTEGENRTRIYNRRS 185

RESULTS 14
US-10-083-336A-2
; Sequence 2, Application US/10083336A
; Publication No. US2003018165A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RID 01-58)
; CURRENT APPLICATION NUMBER: US710/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 2
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-2

Query Match          72.7%; Score 748; DB 12; Length 179;
Best Local Similarity 10.0%; Pred. No. 1e-77; Index 0; Gaps 0;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 2 IFPKQYPIINFTTAGATVOSYTNPFRAYGRLLTGADYRHEIPYTPNRYGLPINORFILV 61  
 Db 36 IFPKQYPIINFTTAGATVOSYTNPFRAYGRLLTGADYRHEIPYTPNRYGLPINORFILV 95  
 Qy 62 ELSNHAELSVTALDVNTAVYVGAGRNSAYFPDQNQDAEAITHLFTDVQNYRTFAFG 121  
 Db 96 ELSNHAELSVTALDVNTAVYVGAGRNSAYFPDQNQDAEAITHLFTDVQNYRTFAFG 155  
 Qy 122 GNYDRLEQLAGNLRENTIELGNGPL 145  
 Db 156 GNYDRLEQLAGNLRENTIELGNGPL 179

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RESULT 15  
 US-09-792-793A-39  
 ; Sequence 39, Application US/09792793A  
 ; Patent No. US2003016370A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: McDonald, John R.  
 ; CCGSINS, Philip  
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND OTHER INFLAMMATORY CONDITIONS AND DISORDERS  
 ; FILE REFERENCE: 25020-601D  
 ; CURRENT APPLICATION NUMBER: US/09/792,793A  
 ; CURRENT FILING DATE: 2001-02-22  
 ; NUMBER OF SEQ ID NOS: 93  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 39  
 ; LENGTH: 247  
 ; TYPE: PRT  
 ; ORGANISM: Trichosanthus kirilowii  
 ; US-09-792-793A-39

Query Match 33.2%; Score 342; DB 10; Length 247;  
 Best Local Similarity 39.5%; Pred. No. 8e-31;  
 Matches 73; Conservative 46; Mismatches 54; Indels 12; Gaps 5;  
 Qy 10 INFPTAGATVOSYTNPFRAYGRLLTGADYRHEIPYTPNRYGLPINORFILVSNHAEL 69  
 Db 2 VSFRLSGATSSSYGVISNRKALPNERKL-YD-PLL--RSLSLPSQRVALIHLINYADE 58  
 Qy 70 SVTLALDVNTAVYVGAGRNSAYFPDQNQDAEAITHLFTDVQNYRTFAFGNNYDLE 128  
 Db 59 TISVALDVNTVYIMGRAGDSYFF--NPSATAAKCYFDAMKVTFPLPSENYERIQ 115  
 Qy 129 QLAGNLRENTIELGNGPLEEIASLYYYSTGGTQLPTLARSFIICOMISBEARQYIEQE 188  
 Db 116 TAAGKIRENTIELGNPLALDSATLLEFYNNAN----SAASALMVLQIQTSEARYKFIEQ 170  
 Qy 189 MRTRI 193  
 Db 171 IGKRV 175

Search completed: February 10, 2004, 16:53:55  
 Job time : 26.7969 secs

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: February 10, 2004, 16:17:35 ; Search time 10.8228 Seconds  
(without alignments)  
1777.145 Million cell updates/sec

Title: US-10-083-336A-10  
Perfect score: 1029  
Sequence: 1 MIFPKQYIPLNFTTAGATVQ.....RFQYIEGMRTRIYNRSA 200

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs., 96168682 residues

Total number of hits satisfying chosen parameters:

283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

PIR\_76.\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	1024		99.5	576	1 RLCSD	ricin D precursor
2	934.5		90.8	564	1 RLCAG	agglutinin precursor
3	353.5		34.4	528	2 S32431	abrin-d precursor
4	353.5		34.4	562	2 S16022	abrin-c precursor
5	345		33.5	527	2 S32430	abrin-b precursor
6	342		33.2	289	1 RLTZT	rrRNA N-Glycosidase
7	338		32.8	247	2 JU0393	karasurin - Mongolian
8	338		32.8	247	2 JC5032	karasurin-B - Tric
9	338		32.8	289	2 JC5606	karasurin C - Tric
10	336.5		32.7	251	2 C39761	abrin (clone 7.2)
11	329.5		32.0	528	1 TZLSA	abrin-a precursor
12	300.5		29.9	278	2 S23519	beta-luffin - smooth
13	291		28.3	250	2 JN0108	luffin-b - smooth
14	286		27.8	570	2 S62627	agglutinin I precursor
15	284.5		27.6	277	2 S22494	mistletoe lectin I
16	279		27.1	286	2 S25560	rrRNA N-Glycosidase
17	278		27.0	245	2 JC4840	rrRNA N-Glycosidase
18	277		26.9	286	1 RLUGGG	rrRNA N-Glycosidase
19	272		26.4	286	2 JC4235	rrRNA N-Glycosidase
20	245		23.9	316	2 JT0753	rrRNA N-Glycosidase
21	197.5		19.2	294	2 S28421	rrRNA N-Glycosidase
22	182		17.7	313	2 S17757	rrRNA N-Glycosidase
23	180.5		17.5	261	2 JB0401	antiviral protein
24	178		17.3	278	2 A39817	rrRNA N-Glycosidase
25	156		15.2	272	2 JC4811	betavulgin - beet
26	149.5		14.5	289	2 T12573	rrRNA N-Glycosidase
27	140		13.6	280	1 RLBH	tritin - wheat
28	137		13.3	275	2 S33631	

## ALIGNMENTS

30	133	12.9	281	2 B38664	30K ribosome inact
31	132	12.8	280	2 JC5848	protein synthesis
32	131	12.7	253	2 S28542	rrNA N-Glycosidase
33	127	12.3	253	2 S28539	rrNA N-Glycosidase
34	127	12.3	253	2 S29931	rrNA N-Glycosidase
35	126	12.2	310	2 S46239	ribosome inactivat
36	124	12.1	283	2 S05205	rrNA N-Glycosidase
37	123.5	12.0	293	2 S17519	rrNA N-Glycosidase
		12.0	253	2 S28541	rrNA N-Glycosidase
		12.1	292	1 RJQBHG2	rrNA N-Glycosidase
		11.2	253	2 A58923	Shiga-like toxin I
		10.8	319	2 B30779	Shiga toxin 2 subu
		10.8	319	2 G35640	Shiga-like toxin 2 subu
		10.7	318	2 S01032	Shiga-like toxin I
		10.7	236	2 S17932	rrNA N-Glycosidase

A;Residues: 315-335, 'N', 337-342, 'NH', 345-362, 364-383, 'PS', 386-399, 'T', 401, 'D', 403, 'E', 405-376, 'F', 529-564, 'W', 566, 'H', 567-570, 'L', 573-574, 'F', <FUN>  
 A;Note: this paper, one of a series, summarizes the experimental details for the determinants of Ricinus communis agglutinin B-chain.  
 R;Ready, M.P.; Kim, Y.; Robertus, J.D.  
 Proteins 10, 270-278, 1991  
 A;Title: Site-directed mutagenesis of ricin A-chain and implications for the mechanism of action.  
 A;Reference number: A48237; PMID:91352006; PMID:1881883  
 A;Contents: annotation; active site  
 R;Katzin, B.J.; Collins, E.J.; Robertus, J.D.  
 Proteins 10, 260-269, 1991  
 A;Title: Structure of ricin B-chain at 2.5 angstrom resolution.  
 A;Reference number: A48238; PMID:1881882  
 A;Contents: annotation; X-ray crystallography, 2.5 angstroms  
 C;Comment: The functional molecule is a disulfide-linked dimer of A and B chains, which inactivates the 60S ribosomal subunit.  
 C;Comment: The A chain inhibits protein synthesis; it is also responsible for cell agglutination (lectin).  
 C;Comment: This protein is cytotoxic and very poisonous to animals.  
 C;Superfamily: ricin; rRNA N-glycosidase homology  
 C;Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; RNA binding; seed  
 F;1-35/Domain: signal sequence #status predicted <SIG>  
 F;36-302/Product: ricin D chain A #status experimental <ACH>  
 F;46-293/Domain: rRNA N-glycosidase homology <RNG>  
 F;315-576/Product: ricin D chain B #status experimental <BCH>  
 F;331-373,377-414,417-455,462-497,501-540,543-576/Region: 40-residue repeats  
 F;45,409-449/Banding site: carbohydrate (Asn) (covalent)  
 F;115,158,243,244/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted  
 F;212/Active site: Glu #status experimental  
 F;294-318,-343,-377-394,-465-478,-504-521/Disulfide bonds: #status experimental  
 F;336,349,360/Banding site: N-acetylgalactosamine (Asp, Gln, Asn) #status experimental  
 F;548,569/Binding site: N-acetylgalactosamine (Asp, Asn) #status experimental  
 Query Match 99%; Score 1024; DB 1; Length 575;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-84;  
 Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 2 1FPKQPIINFTAGATVQSTKTFNTRAVGRGLTTGADVRHELPVLPNRVLGPINQRFLV 61  
 Db 36 1FPKQPIINFTAGATVQSTKTFNTRAVGRGLTTGADVRHELPVLPNRVLGPINQRFLV 95  
 RESULT 3  
 S32431  
 A;Molecule type: mRNA  
 A;Residues: 1-228 <HUN>  
 A;Cross-references: GB:M98346  
 R;Hung, C.; Lee, M.; Lee, T.; Lin, J.  
 N;Contains: rRNA N-glycosidase (EC 3.2.2.22)  
 C;Species: Abrus precatorius (Indian licorice)  
 C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 16-Jul-1999  
 C;Accession: A24261; A24210  
 R;Roberts, L.M.; Lamb, J.F.; Pappin, D.J.C.; Lord, J.M.  
 J. Biol. Chem. 260, 15682-15686, 1985  
 A;Title: The primary sequence of Ricinus communis agglutinin. Comparison with ricin.  
 A;Reference number: A24261; PMID:2993130  
 A;Accession: A24261  
 A;Molecule type: mRNA  
 A;Residues: 1-564 <ROB>  
 A;Cross-references: GB:M12089; PID:9169700; PID:AAA33869\_1; PID:9169701  
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 Db 640 FOYIEGEMTRIYNRSSA 234<br

F;293-325;326-366,369-407;414-449,453-492,495-528/Region: 40-residue repeats  
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted  
 F;164,167/Active site: Glu, Arg #substrates predicted  
 F;200,201,53,31-401,402/Binding site: carbohydrate (Asn) (covalent)  
 F;247,248,249,346-473/Disulfide bond: #status predicted  
 F;288,312/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted  
 F;500,521/Binding site: N-acetylglactosamine (Asp, Asn) #status predicted

Query Match 34.4%; Score 353.5; DB 2; Length 528;  
 Best Local Similarity 45.5%; Pred. No. 5.1e-24;  
 Matches 86; Conservative 24; Mismatches 70; Indels 9; Gaps 4;

Qy 6 QYPLINFATAGATVQSYTNFIRAVGRGLTTGADVRHEIPVLPNRVLGPINQRFLVELSN 65  
 Db 1 QDQVIKFTEGATOSQYKOFIEALRQLRGG--LHIDIPVLPDPPTVEERNRYITYVLSN 58

Qy 66 HAEISVTLADTNAVYVGIRGNSAYFFHPDNQEADAEATHLTFTDVQNRVTFARGNYD 125  
 Db 59 SERESIEVGIDVTNAVYVAYZGSQSYFL--RDAPASASTYLFPGTQ-RYSLRFDSYV 114

Qy 126 RLEQLAGNLRENIELNGNPLEBAISALYYYSTGGTQPLTLARSFIICOMISEAARFOYI 185  
 Db 115 DLERWAHQTEEVISLGLQALTAIS--FLRGASNDEEKARTLIVITQMASEAAARYI 171

Qy 186 EGEMTRIR 194  
 Db 172 SNRVGSIR 180

RESULT 4  
 abrin-b precursor - Indian licorice  
 N/Contains: rRNA N-glycosidase (EC 3.2.2.22)  
 C;Species: Abrus precatorius (Indian licorice)  
 C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 20-Aug-1999  
 C;Accession: S16022  
 R;Wood, K.A.; Lord, J.M.; Wawrzynczak, E.J.; Piatak, M.  
 R;Biol. J. Biochem. 198; 723-732, 1991  
 A;Title: Preprobrin: genetic cloning, characterisation and the expression of the A-chain  
 A;Reference number: S16022; MUID:91266957; PMID:2050149  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-562 <WOO>  
 A;Cross-references: BML:1X5667; PID:916084; BIDN:CA39302.1; PID:916085  
 C;Comment: Abrin consists of an A chain, which inhibits protein synthesis by inactivating The A and B chains are linked by a single disulfide bond, which is essential for toxic C;Superfamily: ricin; rRNA N-glycosidase homology  
 C;Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; pyroglutamic acid P;35-85/Product: abrin-c chain A #status predicted <ACP>  
 P;41-280/Domain: rRNA N-glycosidase homology <RNG>  
 P;295-562/Product: abrin-c chain B #status predicted <BCH>  
 P;317-359,360-400/Domain: rRNA N-glycosidase homology <RNG>  
 P;35/Modified site: Pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted  
 P;198,201/Active site: Glu, Arg #substrates predicted  
 P;234,237,291,346/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 P;281,283,333-380,451-464,490-507/Disulfide bond: #status predicted  
 P;322,346/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted  
 P;534,555/Binding site: N-acetylglactosamine (Asp, Asn) #status predicted

Query Match 34.4%; Score 353.5; DB 2; Length 562;  
 Best Local Similarity 45.5%; Pred. No. 5.5e-24;  
 Matches 86; Conservative 24; Mismatches 70; Indels 9; Gaps 4;

Qy 6 QYPLINFATAGATVQSYTNFIRAVGRGLTTGADVRHEIPVLPNRVLGPINQRFLVELSN 65  
 Db 35 QDQVIKFTEGATOSQYKOFIEALRQLRGG--LHIDIPVLPDPPTVEERNRYITYVLSN 92

Qy 66 HAEISVTLADTNAVYVGIRGNSAYFFHPDNQEADAEATHLTFTDVQNRVTFARGNYD 125  
 Db 93 SERESIEVGIDVTNAVYVAYZGSQSYFL--RDAPASASTYLFPGTQ-RYSLRFDSYV 148

Qy 126 RLEQLAGNLRENIELNGNPLEBAISALYYYSTGGTQPLTLARSFIICOMISEAARFOYI 185  
 Db 149 DLERWAHQTEEVISLGLQALTAIS--FLRGASNDEEKARTLIVITQMASEAAARYI 205  
 N/Contains: Abrus precatorius - Indian licorice (fragment)  
 C;Species: Abrus N-glycosidase (EC 3.2.2.22)  
 C;Date: 30-Sep-1993 #sequence\_revision 01-Aug-1997 #text\_change 20-Aug-1999  
 C;Accession: S32430; JC1399  
 R;Hung, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.  
 J. Mol. Biol. 229, 263-267, 1993  
 A;Title: Primary structure of three distinct isoabrinns determined by cDNA sequencing. Cor A;Reference number: S32429; MUID:93132798; PMID:8421313  
 A;Molecule type: mRNA  
 A;Cross-references: GB:M98345; NID:9165296; PIDN:AAA32625.1; PID:9166297  
 R;Kimura, M.; Sumizawa, T.; Funatsu, G.  
 Biosci. Biotechnol. Biochem. 57, 166-169, 1993  
 A;Title: The complete amino acid sequences of the B-chains of Abrin-a and Abrin-b, toxic A;Reference number: JC1398; MUID:93169023; PMID:7763422  
 A;Accession: JC1399  
 A;Molecule type: protein  
 A;Residues: 260-281,'D' 283-290,'N' 292-349,'PQ' 352-377,'N' 379-425,'M' 427,'D' 429-430,  
 A;Experimental source: seed  
 C;Superfamily: ricin; rRNA N-glycosidase homology  
 C;Keywords: disulfide bond; duplication; glycoprotein; glycosidase; hydrolase; lectin; P  
 P;1-250/Product: abrin-b chain A #status predicted <ACH>  
 P;7-245/Domain: rRNA N-glycosidase homology <RNG>  
 P;260-527/Product: abrin-b chain B #status experimental <BCH>  
 P;282-324,325-365,368-406,413-448,452-491,444-527/Region: 40-residue repeats  
 P;1/Modified site: Pyrrolidone carboxylic acid (Gln) #status predicted  
 P;74,113,194-195/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted  
 P;110,350,400/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 P;163-166/Active site: Glu, Arg #status predicted  
 P;246,268,285-304,328-345,416-429,455-472/Disulfide bonds: #status predicted  
 P;287,311/Binding site: N-acetylglactosamine (Asp, Asn) #status predicted  
 P;499,520/Binding site: N-acetylglactosamine (Asp, Asn) #status predicted  
 Query Match 33.5%; Score 345; DB 2; Length 527;  
 Best Local Similarity 45.5%; Pred. No. 3e-23; Mismatches 72; Indels 10; Gaps 4;  
 Matches 87; Conservative 22; Mismatches 72; Indels 10; Gaps 4;

Qy 6 QYPLINFATAGATVQSYTNFIRAVGRGLTTGADVRHEIPVLPNRVLGPINQRFLVELSN 65  
 Db 1 QDQVIKFTEGATOSQYKOFIEALRQLRGG--LHIDIPVLPDPPTVEERNRYITYVLSN 58  
 Qy 66 HAEISVTLADTNAVYVGIRGNSAYFFHPDNQEADAEATHLTFTDVQNRVTFARGNYD 125  
 Db 59 SDTESIAGIDSVNATVATRAGNSYFL--RDAPTSASVPLFGTQ-QYSLRENGSYI 114  
 Qy 126 RLEQLAGNLRENIELNGNPLEBAISALYYYSTGGTQPLTLARSFIICOMISEAARFOYI 185  
 Db 115 DLERWAHQTEEVISLGLQALTAIS--QSGTDDQEARTLIVITQMASEAAARYF1 170  
 Query Match 34.4%; Score 353.5; DB 2; Length 562;  
 Best Local Similarity 45.5%; Pred. No. 5.5e-24;  
 Matches 86; Conservative 24; Mismatches 70; Indels 9; Gaps 4;

Qy 186 EGEMTRIR 196  
 Db 171 SYRVGSIR 181

RESULT 6  
 rRNA N-glycosidase (EC 3.2.2.22) alpha-trichosanthin precursor [validated] - Mongolian sr  
 N/Alternative names: alpha-TCS; type I ribosome-inactivating protein  
 C;Species: Trichosanthes kirilowii (Mongolian snake-gourd)

C; Date: 30-Sep-1988 #sequence\_revision 26-Jan-1996 #text\_change 23-Mar-2001  
 C; Accession: JT0566; A36273; JC1093; JT0003  
 R; Shaw, P.-C.; Yang, M.H.; Zhu, R.H.; Ho, W.K.X.; Ng, T.B.; Yeung, H.W.  
 Gene 97, 267-271, 1991  
 A; Title: Cloning of trichosanthin cDNA and its expression in Escherichia coli.  
 A; Reference number: JT0566; MUID:91153657; PMID:1999291  
 A; Accession: JT0566.  
 A; Molecule type: mRNA  
 A; Residues: 1-289 <SHA>  
 A; Cross-references: GB:M34858; NID:9170536; PID:9170537  
 A; Experimental source: tuber  
 R; Chow, T.P.; Feldman, R.A.; Lovett, M.; Piatak, M.  
 J. Biol. Chem. 265, 8670-8674, 1990  
 A; Isolation and DNA sequence of a gene encoding alpha-trichosanthin, a type I rib  
 A; Reference number: A36274; MUID:90256790; PMID:2341400  
 A; Accession: A36274  
 A; Molecule type: DNA  
 A; Residues: 1-233, 'T', 235-246, 'W', 248-289 <CHO>  
 A; Cross-references: GB:J0544; NID:9105334; PID:AAA34206.1; PMID:9170535  
 R; Zheng, H.G.; Wang, B.; Shao, P.Z.; Yang, X.R.  
 Acta Genet. Sin. 21, 42-51, 1994  
 A; Title: Cloning and DNA sequencing of the gene encoding Trichosanthin.  
 A; Reference number: JC1093; MUID:94271613; PMID:8003348  
 A; Accession: JC1093  
 A; Molecule type: DNA  
 A; Residues: 1-72, 'V', 74-90, 'S', 92-233, 'T', 235-267, 'D', 269-289 <ZHE>  
 A; Cross-references: GB:S7-0176; NID:9547148; PID:ABA1048.1; PMID:9547149  
 R; Collins, E.J.; Robertus, J.D.; Lopresti, M.; Stone, K.L.; William, K.R.; Wu, P.; Yuan  
 J. Biol. Chem. 265, 8665-8669, 1990  
 A; Title: Primary amino acid sequence of alpha-trichosanthin and molecular models for abr  
 A; Reference number: A36273; MUID:90256789; PMID:2341399  
 A; Accession: A36273  
 A; Molecule type: protein  
 A; Residues: 24-270 <COL>  
 A; Residues: 24-56, 'L', 58-59, 'I', 61-71, 'I', 73-81, 85-86, 'L', 88-92, 'DAGLPNAVL', 93-142, 'GL'  
 A; Experimental source: tuber  
 R; Huang, Q.; Liu, S.; Tang, Y.; Jin, S.; Wang, Y.  
 submitted to the Brookhaven Protein Data Bank, July 1994  
 A; Reference number: A67091; PDB:1BPK  
 A; Contents: annotation; X-ray crystallography, 1.6 angstroms, with adenine, residues 24-  
 R; Huang, Q.; Liu, S.; Tang, Y.; Jin, S.; Wang, Y.  
 submitted to the Brookhaven Protein Data Bank, July 1994  
 A; Reference number: A67032; PDB:1MKK  
 A; Contents: annotation; X-ray crystallography, 1.6 angstroms, with formycin, residues 24-  
 R; Xiong, J.P.; Xia, Z.X.; Wang, Y.  
 submitted to the Brookhaven Protein Data Bank, December 1994  
 A; Contents: annotation; X-ray crystallography, 1.7 angstroms, with NADPH, residues 24-27  
 R; Xiong, J.P.; Xia, Z.X.; Wang, Y.  
 Nat. Struct. Biol. 1, 695-700, 1994  
 A; Reference number: A58622; MUID:95360714; PMID:1634073  
 A; Comment: annotation; X-ray crystallography, 1.7 angstroms  
 C; Comment: Alpha-trichosanthin has been used to induce abortions.  
 C; Genetics:  
 A; Function:  
 A; Description: hydrolyzes the N-glycosidic bond of a specific adenosine in 28S rRNA ther  
 C; Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology  
 C; Keywords: abortifacient; glycosidase; hydrolase; root; toxin  
 F; 1-23(Domain: signal sequence #status predicted <SIG>  
 F; 24-27(Domain: trichosanthin alpha #status predicted <MAT>  
 F; 27-56(Domain: rRNA N-glycosidase homology <RNG>  
 F; 271-289(Domain: carboxyl terminal propeptide #status predicted <CTP>  
 F; 93, 183, 186/Active site: Tyr, Glu, Arg #status predicted  
 C; Query Match 33.2%; Score 342; DB 1; Length 289;

Best Local Similarity 39.5%; Pred. No. 2.6e-23;  
 Matches 73; Conservative 46; Mismatches 54; Indels 12; Gaps 5;  
 Qy 10 INFATGATVOSYTINFIRAVGRGLTGAIVRHEIPVLPNRYGLPINQRFLVLSNHAEI 69  
 Db 25 VSFRLSGATSSSSYGVFTSNLKALPNERKL-YDPLL--RSSLPGSQRAYLTHLYADE 81  
 Qy 70 SVTLALDVNTAATVGYGRAGNSAYFFHDQEDAAITHLFTDVQNYTFAGGGNYDRL 128  
 Db 82 TISVAIDTVNTVYMGTRGDTYFF --NEASATEAKYVFDAKRTVLPYSGNERLQ 138  
 Qy 129 QLAGNLRENTIELNGNPLEAISALYYSTTGQLPLARSFLICQIMSEARFQYEGE 188  
 Db 139 TAAGKIRENTIPLGLPALSATLTLYNNAN----SAASALMVLQTSSEARYKFIEQQ 193  
 A; Reference number: A36274; MUID:92005921; PMID:1914000  
 RESULT 7  
 JU0393 Karasurin - Mongolian snake-gourd  
 C; Species: Trichosanthes kirilowii (Mongolian snake-gourd)  
 C; Date: 30-Sep-1991 #Sequence\_revision 30-Sep-1991 #text\_change 12-Apr-1995  
 C; Accession: JU0393; BS0163  
 R; Toyofawa, S.; Takeki, T.; Karo, Y.; Ogihara, Y.  
 Chem. Pharm. Bull. 39, 1244-1244, 1991  
 A; Title: The complete amino acid sequence of an abortifacient protein, karasurin.  
 A; Reference number: JU0393; MUID:92005921; PMID:1914000  
 A; Accession: JU0393  
 A; Molecule type: protein  
 A; Residues: 1-247 <TOY>  
 A; Note: a sequence which lacks Ala-247 is also shown in this publication  
 C; Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology  
 C; Keywords: abortifacient  
 F; 4/243/Domain: rRNA N-glycosidase homology <RNG>  
 Query Match 32.8%; Score 338; DB 2; Length 247;  
 Best Local Similarity 40.0%; Pred. No. 4.8e-23;  
 Matches 74; Conservative 46; Mismatches 53; Indels 12; Gaps 5;  
 Qy 10 INFATGATVOSYTINFIRAVGRGLTGAIVRHEIPVLPNRYGLPINQRFLVLSNHAEI 69  
 Db 2 VSFRLSGATSSSSYGVFTSNLKALPNERKL-YDPLL--RSSLPGSQRAYLTHLYADE 58  
 Qy 70 SVTLALDVNTAATVGYGRAGNSAYFFHDQEDAAITHLFTDVQNYTFAGGGNYDRL 128  
 Db 59 TISVAIDTVNTVYMGTRGDTYFF --NEASATEAKYVFDAKRTVLPYSGNERLQ 115  
 Qy 129 QLAGNLRENTIELNGNPLEAISALYYSTTGQLPLARSFLICQIMSEARFQYEGE 188  
 Db 116 TAAGKIRENTIPLGLPALSATLTLYNNAN----SAASALMVLQTSSEARYKFIEQQ 170  
 A; Reference number: A66711; PDB:1ITCS  
 RESULT 8  
 JC5032 Karasurin-B - Trichosanthes kirilowii var. japonica  
 C; Species: Trichosanthes kirilowii var. japonica  
 C; Date: 27-Feb-1997 #Sequence\_revision 27-Feb-1997 #text\_change 23-May-1997  
 C; Accession: JC5032  
 R; Kondo, T.; Mizukami, H.; Takeda, T.; Ogihara, Y.  
 Biol. Pharm. Bull. 19, 1485-1489, 1996  
 A; Title: Amino acid sequences and ribosome-inactivating activities of karasurin-B and ka  
 A; Reference number: JC5032; MUID:97108848; PMID:8951169  
 A; Accession: JC5032  
 A; Status: Preliminary  
 A; Molecule type: protein  
 A; Residues: 1-247 <KON>

C;Comment: This protein belongs to type I ribosomal-inactivating proteins which catalyze  
C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology <RNG>  
F;4-243/Domain: rRNA N-glycosidase homology

Query Match 32.8%; Score 338; DB 2; Length 247;  
Best Local Similarity 40.0%; Pred. No. 4.8e-23;  
Matches 74; Conservative 46; Mismatches 53; Indels 12; Gaps 5;

Qy 10 INFPTAGATQSYTNTPIRAVGRLLTGADYHEIPVLPNVLINQRFLVLELSNHAEL 69  
2 VSFRLSATSSSYGVTSNKLAPYERKL-YDIPLU-RSTLPGSQRVALIHLINYADE 58

Db 70 SVTILADVTNAYVVGKAGRNSAYFFHPDNQEDA-EAITHLTDVQNYRTFAFGNNYDRLE 128  
59 TISVALDTVNAYVMGTRAGDTSYFF--NEASATEAKYVKDARKVTLPLPSGNVERLQ 115

Qy 129 QLAGNRNENIEGGNGPLEIAISALYYSTGGTQLPILTARSFLICOMISEARFQYIEGE 188  
116 TAGKIRENIPPLGLPAUDSAITLFLYNNAN----SAASALMVLQSTSEARRYKTEEQ 170

Qy 189 MTRI 193  
Db 171 IGKRV 175

RESULT 9

JCS606 Karasurin C - Trichosanthes kirilowii var. japonica  
N;Contains: karasurin A  
C;Species: Trichosanthes kirilowii var. japonica  
C;Date: 23-Sep-1997 #sequence\_revision 23-Sep-1997 #text\_change 19-Jul-2002  
C;Accession: JCS606; JCS033  
R;Mizukami, H.; Iida, K.; Kondo, T.; Ogihara, Y.  
Biol. Pharm. Bull. 20, 711-713, 1997  
A;Title: Cloning and bacterial expression of a gene encoding ribosome-inactivating protein  
A;Reference number: JCS606; MUID:92129984; PMID:97356562; PMID:9212998  
A;Accession: JCS606  
A;Molecule type: DNA  
A;Residues: 1-289 <MTZ>  
A;Cross-references: DDBJ:AB000666; NID:92329830; PID:BAAA21786.1; PID:g2329831  
R;Kondo, T.; Mizukami, H.; Takeda, T.; Ogihara, Y.  
Biol. Pharm. Bull. 19, 1485-1489, 1996  
A;Title: Amino acid sequences and ribosome-inactivating activities of karasurin-B and ka  
A;Reference number: JCS532; MUID:97108848; PMID:8951169  
A;Accession: JCS532  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 22-270 <KON>  
C;Comment: This protein is a ribosome-inactivating protein and exhibit cytotoxic, abortifacient and anti-tumor activities.  
C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology  
F;22-270/Domain: karasurin C #status predicted <MAC>  
F;24-270/Domain: karasurin A #status predicted <MAA>  
F;27-266/Domain: rRNA N-glycosidase homology <RNG>

Query Match 32.8%; Score 338; DB 2; Length 289;  
Best Local Similarity 40.0%; Pred. No. 5.9e-23;  
Matches 74; Conservative 46; Mismatches 53; Indels 12; Gaps 5;

Qy 10 INFPTAGATQSYTNTPIRAVGRLLTGADYHEIPVLPNVLINQRFLVLELSNHAEL 69  
25 VSFRLSATSSSYGVTSNKLAPYERKL-YDIPLU-RSTLPGSQRVALIHLINYADE 81

Db 70 SYTILADVTNAYVVGKAGRNSAYFFHPDNQEDA-EAITHLTDVQNYRTFAFGNNYDRLE 128  
82 TISVAIDVTNAYVMGTRAGDTSYFF--NEASATEAKYVKDARKVTLPLPSGNVERLQ 138

Qy 129 QLAGNRNENIEGGNGPLEIAISALYYSTGGTQLPILTARSFLICOMISEARFQYIEGE 188  
139 TAGKIRENIPPLGLPAUDSAITLFLYNNAN----SAASALMVLQSTSEARRYKTEEQ 193

Qy 189 MTRI 193

Db 194 IGKRV 198

RESULT 10

C39761 abrin (clone 7.2) precursor - Indian licorice (fragment)  
N;Contains: rRNA N-glycosidase (EC 3.2.2.22)  
C;Species: Abrus precatorius (Indian licorice)  
C;Accession: C39761; S14471  
R;Evensen, G.; Mathiesen, A.; Sundan, A.  
J. Biol. Chem. 266, 6848-6852, 1991  
A;Title: Direct molecular cloning and expression of two distinct abrin A-chains.  
A;Description: Number: A39761; MUID:91201329; PMID:2016300  
A;Reference number: S14471  
A;Accession: C39761  
A;Molecule type: DNA  
A;Residues: 'N', 1-251 <EV2>  
A;Cross-references: EMBL:X54872; PID:g16088; PID:CAA38654.1; PID:g16089  
A;Cross-references: rRNA N-glycosidase homology  
C;Superfamily: ricin; rRNA N-glycosidase: hydrolase; lectin; toxin  
C;Keywords: duplication; glycosidase; hydrolyase; lectin; toxin  
F;1-251/Domain: abrin (Clone 7.2) chain A #status predicted <ACH>  
F;74-246/Domain: rRNA N-glycosidase homology <RNG>  
F;74-113,195,196/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted  
F;164,167/Active site: Glu, Arg #status predicted

Query Match 32.7%; Score 336.5; DB 2; Length 251;  
Best Local Similarity 44.9%; Pred. No. 6.7e-23;  
Matches 83; Conservative 24; Mismatches 69; Indels 9; Gaps 4;

Qy 10 INFPTAGATQSYTNTPIRAVGRLLTGADYHEIPVLPNVLINQRFLVLELSNHAEL 69  
5 IKESTEGTSOSTKOFTEALRELRGG-LINDIPVLRDPTEVEERNRITYVELNSNRE 62

Db 70 SYTILADVTNAYVVGKAGRNSAYFFHPDNQEDA-EAITHLTDVQNYRTFAFGNNYDRLE 129  
63 SIEVGIDTNAYTAYXRSQSFL--RDAPSASTYLFTGQ-RYSLRFDSGSYDIER 118

Qy 130 LAGNLRENTIELNGNPLERBAISALYYSTGGTQLPILTARSFLICOMISEAARFQYIEGE 189  
Db 119 WAHDTREQISLGQALTHAIS--FLRGASNDKEEKARTLVIVIQMASSEAARTRYISNRV 175

RESULT 11

TZLSA abrin precursor - Indian licorice (fragment)  
N;Contains: rRNA N-glycosidase (EC 3.2.2.22)

C;Species: Abrus precatorius (Indian licorice)  
C;Accession: S32429; JTO202; A39761; JC1398; S14472; S24133; S74110; S74111  
R;Hung, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.  
J. Mol. Biol. 229, 263-267, 1993  
A;Title: Primary structure of three distinct isoabrinins determined by cDNA sequencing. Cor  
A;Reference number: S32429; MUID:93132798; PMID:8421313  
A;Accession: S32429  
A;Residues: nucleic acid sequence not shown

A;Molecule type: mRNA  
A;Cross-references: GB:N98344; PID:g166294; PID:AAA32624.1; PID:g166295  
A;Note: the coding region for the sequence shown is preceded by an ARG codon  
A;Note: residues 1-8 were derived from the synthesized primer  
R;Funatsu, G.; Taguchi, Y.; Kamensono, M.; Yanaka, M.  
Agric. Biol. Chem. 52, 1095-1097, 1988

A;Title: The complete amino acid sequence of the A-chain of abrin-a, a toxic protein from Abrin. Accession number: UTO202  
A;Accession: JTO202  
A;Molecule type: protein  
A;Residues: 1-201-203-251 <PNT>  
A;Note: the amino-terminal residue forms Pyrrolidone carboxylic acid; therefore, we have R;Evensen, G.; Mathiesen, A.; Sundan, A.  
R;Biol. Chem. 266, 6848-6852, 1991  
A;Title: Direct molecular cloning and expression of two distinct abrin A-chains.  
A;Reference number: A39761; MUID:91201329; PMID:2016300  
A;Accession: A39761  
A;Status: nucleic acid sequence not shown  
A;Molecule type: DNA  
A;Residues: 'B', 2-251 <PNT>  
A;Cross-references: GB:X54872  
A;Note: residues 1-8 were derived from the synthesized primer  
R;Kimura, M.; Sumizawa, T.; Funatsu, G.  
Biosci. Biotechnol. Biochem. 57, 166-169, 1993  
A;Reference number: JCI1388; MUID:9169023; PMID:7763422  
A;Contents: seeds  
A;Accession: JCI1388  
A;Molecule type: protein  
A;Residues: 261-347, 'T', 349-351, 'A', 353-357, 'L', 359-528 <KIM>  
A;Experimental source: seed  
R;Evensen, G.; Mathiesen, A.; Sundan, A.  
R;Submitted to the EMBL Data Library, October 1990  
A;Description: Direct molecular cloning of two distinct abrin A-chains.  
A;Reference number: S14471  
A;Accession: S14472  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 'ME', 2-251 <EV2>  
A;Cross-references: EMBL:X34873; NID:916090; PID:CAA38655.1; PMID:916091  
R;Chen, Y.L.; Chow, L.P.; Tsugita, A.; Lin, J.Y.  
FEBS Lett. 309, 115-118, 1992  
A;Title: The complete primary structure of abrin-a B chain.  
A;Reference number: S24133; MUID:92371656; PMID:1505674  
A;Accession: S24133  
A;Molecule type: protein  
A;Residues: 262-297, 'Y', 299-426, 'L', 428-466, 'P', 468-482, 'L', 484-528 <CHE>  
R;Lin, S.H.; Chow, L.P.; Chen, Y.C.; Liaw, Y.C.; Lin, J.Y.  
EUR. J. Biochem. 240, 564-569, 1996  
A;Title: Probing the domain structure of abrin-a by tryptic digestion.  
A;Reference number: S74110; MUID:97008945; PMID:8856055  
A;Accession: S74110  
A;Molecule type: protein  
A;Residues: 89-108-154-172 <LIN>  
A;Experimental source: seed  
A;Accession: S74111  
A;Molecule type: protein  
A;Residues: 262-276, 'X', 278-280; 329-346; 369-388; 399-418 <LIN>  
A;Experimental source: seed  
C;Comment: Abrin-a is more toxic than ricin. The toxin consists of an A chain, which contains receptors on the cell surface. The A and B chains are linked by a single disulfide bond.  
C;Superfamily: Ricin; RNA N-glycosidase homology  
C;Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; pyroglutamic acid F;1-251/Product: abrin-a chain A #status experimental <ACH>  
F;7-246/Domain: rRNA N-glycosidase homology <RNG>  
F;261-528/Product: abrin-a chain B #status experimental <BCH>  
F;283-325-326-366, 369-407, 414-449, 453-493, 495-528/Region: 40-residue repeats F;1/Modified site: Pyrrolidone carboxylic acid (Gln) #status experimental  
F;164-167/Active site: Glu, Arg #status predicted  
F;247-269, 286-305, 329-346, 417-430, 456-473/Disulfide bonds: #status predicted F;288-312/Binding site: N-acetyl galactosamine (Asp, Asn) #status predicted F;361-401/Binding site: carbohydrate (Asn) (covalent) #status experimental F;500-521/Binding site: N-acetyl galactosamine (Asp, Asn) #status predicted

Query Match 32.0%; Score 329.5; DB 1; Length 528;  
Best Local Similarity 42.8%; Pred. No. 7.5e-22; Mismatches 28; Indels 13; Gaps 5;

Qy 10 INFETTAGATVOSYTNTFIRAVGRGLTQDVRHEIPVNLPIVNPRLPINOFLIVLSNHAEL 69  
Db 5 IKSTEGATQSQTQKFELALRERLGG-LHIDIPVDPDTIQLQERNYITVLSNSDE 62  
Qy 70 SIVTLALWNTNAYVGVYDAGNSAYFFH -PDNQEDAAEATHLFTDVQNRYTFAGGNNDRL 127  
Db 63 SIEVGIDVNTNAYVAVYGTQSFLRDPSASSD---YLFTGTD-QHSLPFYGTGDL 116  
Qy 128 EQALGNRLNIELNGPBEIASLYYYSTGTQPLPTLARSFLICIONMSEARFOYLEG 187  
Db 117 ERWAHQSCQIPLGLQALTHGIS---FRRSGNDNEEFKARTLIVIQNVAEARFRYISN 173  
Qy 188 EMTRIR 194  
Db 174 RVRSIQ 180  
  
**RESULT 12**  
S23519  
C;Species: Luffa cylindrica (smooth loofah)  
C;Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 20-Aug-1999  
C;Accession: S23519; S2113  
R;Kataoka, J.; Habuka, N.; Miyano, M.; Matsuta, C.; Kawai, A.  
Plant Mol. Biol. 19, 887-889, 1992  
A;Title: Nucleotide sequence of cDNA encoding beta-luffin, another ribosome-inactivating protein  
A;Reference number: S23519; MUID:92353400; PMID:1643290  
A;Accession: S23519  
A;Molecule type: mRNA  
A;Residues: 1-278 <CAT>  
A;Cross-references: EMBL:X62372; NID:919149; PID:CAA44230.1; PMID:g19150  
C;Superfamily: rRNA N-glycosidase homology  
F;26-264/Domain: rRNA N-glycosidase homology <RNG>  
Query Match 29.9%; Score 307.5; DB 2; Length 278;  
Best Local Similarity 35.8%; Pred. No. 3.2e-20; Mismatches 45; Indels 11; Gaps 3;  
Matches 67; Conservative 45;  
C;Accession: S23519  
Qy 10 INFETTAGATVOSYTNTFIRAVGRGLTQDVRHEIPVNLPIVNPRLPINOFLIVLSNHAEL 69  
Db 24 VSFSLSGADSKSYSKFTALKALPSKEVSMNPLPSAGA---SRYILMQLSNYDAK 80  
Qy 70 SIVTLALWNTNAYVGVYDAGNSAYFFHDDNOEDAETHLFTDVQNRYTFAGGNYDLEQ 129  
Db 81 AIMTAIDYTVNTVMTGVLNVNTGFLVSPGNYELQN 137  
Qy 130 LAGNLRLNIELNGPBEIASLYYYSTGTQPLPTLARSFLICIONMSEARFOYLEG 189  
Db 138 AAQKVREKPLGFRAFDTSALSLFYHD5 ----TAAAGAFLVIIQTTAEASRFYIGQI 192  
Qy 190 RTRTRYN 196  
Db 193 IERPKN 199  
  
**RESULT 13**  
JN0108  
luffin-b - smooth loofah  
C;Species: Luffa cylindrica (smooth loofah)  
C;Date: 04-Sep-1998 #sequence\_revision 04-Sep-1998 #text\_change 07-May-1999  
C;Accession: JN0108  
R;Islam, M.R.; Hirayama, H.; Funatsu, G.  
Agric. Biol. Chem. 55, 229-238, 1991  
A;Title: Complete amino acid sequence of luffin-b, a ribosome-inactivating protein from Luffa cylindrica  
A;Accession: JN0108  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-250 <ISL>  
C;Superfamily: rRNA N-glycosidase homology  
C;Keywords: Luffa cylindrica (smooth loofah)  
C;Accession: JN0108  
F;7-246/Domain: rRNA N-glycosidase homology <RNG>  
F;283-325-326-366, 369-407, 414-449, 453-493, 495-528/Region: 40-residue repeats F;1/Modified site: Pyrrolidone carboxylic acid (Gln) #status experimental  
F;164-167/Active site: Glu, Arg #status predicted  
F;247-269, 286-305, 329-346, 417-430, 456-473/Disulfide bonds: #status predicted F;288-312/Binding site: N-acetyl galactosamine (Asp, Asn) #status predicted F;361-401/Binding site: carbohydrate (Asn) (covalent) #status experimental F;500-521/Binding site: N-acetyl galactosamine (Asp, Asn) #status predicted

Query Match 29.2%; Score 300.5; DB 2; Length 250;